

6	62	SEQ ID NO: 7425	1.6 %	90
7	1190	SEQ ID NO: 7426	1.6 %	90
8	1284	SEQ ID NO: 7427	1.6 %	90
9	3284	SEQ ID NO: 7428	1.6 %	90
10	2921	SEQ ID NO: 7429	1.2 %	67.5
11	349	SEQ ID NO: 7430	0.8 %	45
12	789	SEQ ID NO: 7431	0.8 %	45
13	1185	SEQ ID NO: 7432	0.8 %	45
14	4184	SEQ ID NO: 7433	0.8 %	45
15	1313	SEQ ID NO: 7434	0.64 %	36
16	3948	SEQ ID NO: 7435	0.48 %	27
17	149	SEQ ID NO: 7436	0.44 %	25
18	941	SEQ ID NO: 7437	0.44 %	25
19	1390	SEQ ID NO: 7438	0.44 %	25
20	1613	SEQ ID NO: 7439	0.44 %	25

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	1010	SEQ ID NO: 7440	1.48 %	180
2	3155	SEQ ID NO: 7441	1.48 %	180
3	1229	SEQ ID NO: 7442	1.23 %	150
4	2405	SEQ ID NO: 7443	0.88 %	108
5	2	SEQ ID NO: 7444	0.74 %	90
6	2304	SEQ ID NO: 7445	0.74 %	90
7	2358	SEQ ID NO: 7446	0.74 %	90
8	3160	SEQ ID NO: 7447	0.74 %	90
9	3771	SEQ ID NO: 7448	0.74 %	90
10	4007	SEQ ID NO: 7449	0.74 %	90
11	3079	SEQ ID NO: 7450	0.66 %	81
12	4045	SEQ ID NO: 7451	0.66 %	81
13	1081	SEQ ID NO: 7452	0.49 %	60
14	3268	SEQ ID NO: 7453	0.49 %	60
15	4144	SEQ ID NO: 7454	0.49 %	60
16	614	SEQ ID NO: 7455	0.37 %	45
17	728	SEQ ID NO: 7456	0.37 %	45
18	1537	SEQ ID NO: 7457	0.37 %	45
19	313	SEQ ID NO: 7458	0.32 %	40
20	1744	SEQ ID NO: 7459	0.32 %	40

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	62	SEQ ID NO: 7460	4.44 %	540
2	2151	SEQ ID NO: 7461	2.46 %	300
3	633	SEQ ID NO: 7462	2.22 %	270
4	1158	SEQ ID NO: 7463	2.22 %	270
5	2565	SEQ ID NO: 7464	2.22 %	270
6	2298	SEQ ID NO: 7465	1.77 %	216
7	3159	SEQ ID NO: 7466	1.11 %	135
8	640	SEQ ID NO: 7467	0.98 %	120
9	2186	SEQ ID NO: 7468	0.74 %	90
10	3869	SEQ ID NO: 7469	0.74 %	90
11	2308	SEQ ID NO: 7470	0.66 %	81
12	786	SEQ ID NO: 7471	0.55 %	67.5
13	749	SEQ ID NO: 7472	0.49 %	60
14	1080	SEQ ID NO: 7473	0.49 %	60
15	2358	SEQ ID NO: 7474	0.49 %	60
16	3955	SEQ ID NO: 7475	0.49 %	60
17	714	SEQ ID NO: 7476	0.37 %	45
18	1081	SEQ ID NO: 7477	0.37 %	45
19	1170	SEQ ID NO: 7478	0.37 %	45
20	1228	SEQ ID NO: 7479	0.37 %	45

HLA A24 - 9 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	3797	SEQ ID NO: 7480	37.57 %	600
2	4202	SEQ ID NO: 7481	37.57 %	600
3	3189	SEQ ID NO: 7482	25.05 %	400
4	1864	SEQ ID NO: 7483	23.14 %	369.6
5	1066	SEQ ID NO: 7484	22.54 %	360
6	2143	SEQ ID NO: 7485	22.54 %	360
7	2693	SEQ ID NO: 7486	22.54 %	360
8	1426	SEQ ID NO: 7487	18.78 %	300
9	1238	SEQ ID NO: 7488	18.03 %	288
10	3768	SEQ ID NO: 7489	18.03 %	288
11	797	SEQ ID NO: 7490	15.03 %	240

12	1882	SEQ ID NO: 7491	15.03 %	240
13	1490	SEQ ID NO: 7492	13.77 %	220
14	2237	SEQ ID NO: 7493	13.77 %	220
15	95	SEQ ID NO: 7494	12.52 %	200
16	1821	SEQ ID NO: 7495	12.52 %	200
17	2289	SEQ ID NO: 7496	12.52 %	200
18	3080	SEQ ID NO: 7497	12.52 %	200
19	3660	SEQ ID NO: 7498	12.52 %	200
20	4354	SEQ ID NO: 7499	12.52 %	200

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	2143	SEQ ID NO: 7500	37.87 %	604.8
2	1159	SEQ ID NO: 7501	26.30 %	420
3	1650	SEQ ID NO: 7502	26.30 %	420
4	1150	SEQ ID NO: 7503	18.78 %	300
5	2763	SEQ ID NO: 7504	18.78 %	300
6	3165	SEQ ID NO: 7505	18.78 %	300
7	3201	SEQ ID NO: 7506	15.03 %	240
8	3694	SEQ ID NO: 7507	15.03 %	240
9	4204	SEQ ID NO: 7508	15.03 %	240
10	1692	SEQ ID NO: 7509	13.77 %	220
11	797	SEQ ID NO: 7510	12.52 %	200
12	1610	SEQ ID NO: 7511	12.52 %	200
13	1789	SEQ ID NO: 7512	12.52 %	200
14	1881	SEQ ID NO: 7513	12.52 %	200
15	3090	SEQ ID NO: 7514	12.52 %	200
16	3763	SEQ ID NO: 7515	12.52 %	200
17	2569	SEQ ID NO: 7516	11.27 %	180
18	194	SEQ ID NO: 7517	9.39 %	150
19	1771	SEQ ID NO: 7518	9.39 %	150
20	2488	SEQ ID NO: 7519	9.39 %	150

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	2308	SEQ ID NO: 7520	0.20 %	8144.13515256
2	3729	SEQ ID NO: 7521	0.10 %	4047.23088

3	3574	SEQ ID NO: 7522	0.09 %	3547.4996634
4	3615	SEQ ID NO: 7523	0.06 %	2722.682592
5	3159	SEQ ID NO: 7524	0.05 %	1999.734264
6	2339	SEQ ID NO: 7525	0.03 %	1551.92907744
7	2201	SEQ ID NO: 7526	0.03 %	1521.53694
8	3559	SEQ ID NO: 7527	0.02 %	1174.38939504
9	3085	SEQ ID NO: 7528	0.02 %	1146.296448
10	4070	SEQ ID NO: 7529	0.02 %	970.4103696
11	3708	SEQ ID NO: 7530	0.02 %	958.92888
12	3098	SEQ ID NO: 7531	0.02 %	942.678
13	1362	SEQ ID NO: 7532	0.02 %	900.6984
14	3563	SEQ ID NO: 7533	0.01 %	735.86016
15	3774	SEQ ID NO: 7534	0.01 %	687.655656
16	4242	SEQ ID NO: 7535	0.01 %	685.78272
17	2340	SEQ ID NO: 7536	0.01 %	668.37342936
18	650	SEQ ID NO: 7537	0.01 %	640.1983392
19	3862	SEQ ID NO: 7538	0.01 %	620.57772
20	2860	SEQ ID NO: 7539	0.01 %	607.88448

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	2307	SEQ ID NO: 7540	0.40 %	15915.66281448
2	2201	SEQ ID NO: 7541	0.12 %	4772.09313
3	3558	SEQ ID NO: 7542	0.05 %	2295.04855632
4	1772	SEQ ID NO: 7543	0.04 %	1759.6656
5	3087	SEQ ID NO: 7544	0.03 %	1215.76896
6	2339	SEQ ID NO: 7545	0.02 %	1116.29986272
7	2308	SEQ ID NO: 7546	0.02 %	970.14776112
8	3061	SEQ ID NO: 7547	0.02 %	836.2525104
9	2748	SEQ ID NO: 7548	0.01 %	726.706344
10	3837	SEQ ID NO: 7549	0.01 %	720.8292
11	59	SEQ ID NO: 7550	0.01 %	650.3112
12	2877	SEQ ID NO: 7551	0.01 %	620.22996
13	4114	SEQ ID NO: 7552	0.01 %	559.8936
14	805	SEQ ID NO: 7553	0.01 %	484.4565072
15	1655	SEQ ID NO: 7554	0.01 %	437.48208
16	611	SEQ ID NO: 7555	0.00 %	319.9392
17	1961	SEQ ID NO: 7556	0.00 %	305.94186

18	1223	SEQ ID NO: 7557	0.00 %	289.08792
19	852	SEQ ID NO: 7558	0.00 %	285.67242
20	2139	SEQ ID NO: 7559	0.00 %	284.845869

HLA A 1101 - 9 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	4200	SEQ ID NO: 7560	50 %	18
2	281	SEQ ID NO: 7561	25 %	9
3	3236	SEQ ID NO: 7562	25 %	9
4	509	SEQ ID NO: 7563	16.66 %	6
5	848	SEQ ID NO: 7564	16.66 %	6
6	2193	SEQ ID NO: 7565	16.66 %	6
7	3542	SEQ ID NO: 7566	16.66 %	6
8	541	SEQ ID NO: 7567	15 %	5.4
9	1748	SEQ ID NO: 7568	12.5 %	4.5
10	829	SEQ ID NO: 7569	11.11 %	4
11	1149	SEQ ID NO: 7570	11.11 %	4
12	2027	SEQ ID NO: 7571	11.11 %	4
13	2576	SEQ ID NO: 7572	11.11 %	4
14	873	SEQ ID NO: 7573	8.33 %	3
15	2725	SEQ ID NO: 7574	8.33 %	3
16	3541	SEQ ID NO: 7575	8.33 %	3
17	1837	SEQ ID NO: 7576	7.5 %	2.7
18	2475	SEQ ID NO: 7577	7.5 %	2.7
19	2703	SEQ ID NO: 7578	7.5 %	2.7
20	1823	SEQ ID NO: 7579	6.66 %	2.4

HLA A 1101 - 10 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	3541	SEQ ID NO: 7580	50 %	18
2	281	SEQ ID NO: 7581	25 %	9
3	1495	SEQ ID NO: 7582	25 %	9
4	2303	SEQ ID NO: 7583	25 %	9
5	2616	SEQ ID NO: 7584	25 %	9
6	48	SEQ ID NO: 7585	16.66 %	6
7	1394	SEQ ID NO: 7586	16.66 %	6
8	1499	SEQ ID NO: 7587	16.66 %	6

9	1862	SEQ ID NO: 7588	16.66 %	6
10	1163	SEQ ID NO: 7589	11.11 %	4
11	4006	SEQ ID NO: 7590	11.11 %	4
12	4344	SEQ ID NO: 7591	11.11 %	4
13	633	SEQ ID NO: 7592	10 %	3.6
14	119	SEQ ID NO: 7593	8.33 %	3
15	1190	SEQ ID NO: 7594	8.33 %	3
16	1195	SEQ ID NO: 7595	8.33 %	3
17	1725	SEQ ID NO: 7596	8.33 %	3
18	2728	SEQ ID NO: 7597	8.33 %	3
19	2895	SEQ ID NO: 7598	8.33 %	3
20	3033	SEQ ID NO: 7599	8.33 %	3

HLA B7 - 9 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	1335	SEQ ID NO: 7600	4.44 %	240
2	2580	SEQ ID NO: 7601	4.44 %	240
3	1703	SEQ ID NO: 7602	3.70 %	200
4	113	SEQ ID NO: 7603	2.22 %	120
5	168	SEQ ID NO: 7604	2.22 %	120
6	2842	SEQ ID NO: 7605	2.22 %	120
7	4027	SEQ ID NO: 7606	2.22 %	120
8	3680	SEQ ID NO: 7607	1.66 %	90
9	2085	SEQ ID NO: 7608	1.48 %	80
10	2492	SEQ ID NO: 7609	1.48 %	80
11	2660	SEQ ID NO: 7610	1.48 %	80
12	2906	SEQ ID NO: 7611	1.48 %	80
13	3346	SEQ ID NO: 7612	1.48 %	80
14	4038	SEQ ID NO: 7613	1.48 %	80
15	1163	SEQ ID NO: 7614	1.11 %	60
16	1457	SEQ ID NO: 7615	1.11 %	60
17	2351	SEQ ID NO: 7616	1.11 %	60
18	2471	SEQ ID NO: 7617	1.11 %	60
19	3499	SEQ ID NO: 7618	1.11 %	60
20	3635	SEQ ID NO: 7619	1.11 %	60

HLA B7 - 10 mers	
Maximum possible score using this molecule type	5400

Rank	Start position	Sequence	% of max. score	Score
1	1703	SEQ ID NO: 7620	3.70 %	200
2	17	SEQ ID NO: 7621	2.22 %	120
3	3008	SEQ ID NO: 7622	2.22 %	120
4	4106	SEQ ID NO: 7623	2.22 %	120
5	3450	SEQ ID NO: 7624	1.66 %	90
6	113	SEQ ID NO: 7625	1.48 %	80
7	195	SEQ ID NO: 7626	1.48 %	80
8	307	SEQ ID NO: 7627	1.48 %	80
9	780	SEQ ID NO: 7628	1.48 %	80
10	1000	SEQ ID NO: 7629	1.48 %	80
11	1072	SEQ ID NO: 7630	1.48 %	80
12	1404	SEQ ID NO: 7631	1.48 %	80
13	1980	SEQ ID NO: 7632	1.48 %	80
14	2262	SEQ ID NO: 7633	1.48 %	80
15	2543	SEQ ID NO: 7634	1.48 %	80
16	2906	SEQ ID NO: 7635	1.48 %	80
17	3077	SEQ ID NO: 7636	1.48 %	80
18	3175	SEQ ID NO: 7637	1.48 %	80
19	4195	SEQ ID NO: 7638	1.48 %	80
20	4251	SEQ ID NO: 7639	1.48 %	80

Table 14: Epitopes for SEQ ID NO: 6040

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	20	SEQ ID NO: 7640	0.04 %	2.25
2	91	SEQ ID NO: 7641	0.01 %	1
3	125	SEQ ID NO: 7642	0.01 %	0.75
4	56	SEQ ID NO: 7643	0.00 %	0.5
5	145	SEQ ID NO: 7644	0.00 %	0.5

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	20	SEQ ID NO: 7645	0.01 %	0.9
2	56	SEQ ID NO: 7646	0.00 %	0.5
3	71	SEQ ID NO: 7647	0.00 %	0.5

4	144	SEQ ID NO: 7648	0.00 %	0.5
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HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	115	SEQ ID NO: 7649	0.24 %	30
2	87	SEQ ID NO: 7650	0.04 %	6
3	80	SEQ ID NO: 7651	0.03 %	4.05
4	125	SEQ ID NO: 7652	0.01 %	1.8
5	39	SEQ ID NO: 7653	0.01 %	1.5
6	56	SEQ ID NO: 7654	0.01 %	1.5
7	135	SEQ ID NO: 7655	0.00 %	1.2
8	91	SEQ ID NO: 7656	0.00 %	1
9	119	SEQ ID NO: 7657	0.00 %	1
10	141	SEQ ID NO: 7658	0.00 %	0.9
11	150	SEQ ID NO: 7659	0.00 %	0.6
12	137	SEQ ID NO: 7660	0.00 %	0.54

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	36	SEQ ID NO: 7661	0.24 %	30
2	144	SEQ ID NO: 7662	0.06 %	8
3	101	SEQ ID NO: 7663	0.03 %	4
4	99	SEQ ID NO: 7664	0.02 %	3.6
5	80	SEQ ID NO: 7665	0.02 %	2.7
6	125	SEQ ID NO: 7666	0.01 %	1.6875
7	71	SEQ ID NO: 7667	0.01 %	1.5
8	118	SEQ ID NO: 7668	0.01 %	1.5
9	40	SEQ ID NO: 7669	0.01 %	1.35
10	5	SEQ ID NO: 7670	0.00 %	0.9
11	56	SEQ ID NO: 7671	0.00 %	0.9
12	107	SEQ ID NO: 7672	0.00 %	0.6
13	135	SEQ ID NO: 7673	0.00 %	0.6
14	141	SEQ ID NO: 7674	0.00 %	0.6
15	148	SEQ ID NO: 7675	0.00 %	0.6
16	116	SEQ ID NO: 7676	0.00 %	0.5

HLA A24 - 9 mers				
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Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	153	SEQ ID NO: 7677	1.05 %	16.8
2	80	SEQ ID NO: 7678	0.75 %	12
3	123	SEQ ID NO: 7679	0.50 %	8
4	137	SEQ ID NO: 7680	0.50 %	8
5	9	SEQ ID NO: 7681	0.45 %	7.2
6	77	SEQ ID NO: 7682	0.45 %	7.2
7	112	SEQ ID NO: 7683	0.45 %	7.2
8	73	SEQ ID NO: 7684	0.41 %	6.6
9	32	SEQ ID NO: 7685	0.37 %	6
10	110	SEQ ID NO: 7686	0.37 %	6
11	140	SEQ ID NO: 7687	0.37 %	6
12	143	SEQ ID NO: 7688	0.37 %	6
13	18	SEQ ID NO: 7689	0.30 %	4.8
14	54	SEQ ID NO: 7690	0.30 %	4.8
15	108	SEQ ID NO: 7691	0.30 %	4.8
16	141	SEQ ID NO: 7692	0.30 %	4.8
17	92	SEQ ID NO: 7693	0.27 %	4.4
18	33	SEQ ID NO: 7694	0.25 %	4
19	49	SEQ ID NO: 7695	0.25 %	4
20	111	SEQ ID NO: 7696	0.25 %	4

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	142	SEQ ID NO: 7697	12.52 %	200
2	110	SEQ ID NO: 7698	0.75 %	12
3	99	SEQ ID NO: 7699	0.50 %	8
4	8	SEQ ID NO: 7700	0.45 %	7.2
5	140	SEQ ID NO: 7701	0.45 %	7.2
6	32	SEQ ID NO: 7702	0.37 %	6
7	17	SEQ ID NO: 7703	0.30 %	4.8
8	53	SEQ ID NO: 7704	0.30 %	4.8
9	76	SEQ ID NO: 7705	0.30 %	4.8
10	107	SEQ ID NO: 7706	0.30 %	4.8
11	111	SEQ ID NO: 7707	0.30 %	4.8
12	72	SEQ ID NO: 7708	0.27 %	4.4
13	91	SEQ ID NO: 7709	0.27 %	4.4

14	31	SEQ ID NO: 7710	0.25 %	4
15	127	SEQ ID NO: 7711	0.25 %	4
16	139	SEQ ID NO: 7712	0.25 %	4
17	80	SEQ ID NO: 7713	0.22 %	3.6
18	38	SEQ ID NO: 7714	0.18 %	3
19	118	SEQ ID NO: 7715	0.18 %	3
20	49	SEQ ID NO: 7716	0.12 %	2

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	80	SEQ ID NO: 7717	0.00 %	171.96732
2	147	SEQ ID NO: 7718	0.00 %	51.46848
3	143	SEQ ID NO: 7719	0.00 %	11.6146182
4	56	SEQ ID NO: 7720	0.00 %	11.304684
5	10	SEQ ID NO: 7721	0.00 %	10.34586
6	6	SEQ ID NO: 7722	0.00 %	6.56830734
7	26	SEQ ID NO: 7723	0.00 %	6.07614
8	141	SEQ ID NO: 7724	0.00 %	5.981472
9	148	SEQ ID NO: 7725	0.00 %	5.194044
10	9	SEQ ID NO: 7726	0.00 %	4.299183
11	137	SEQ ID NO: 7727	0.00 %	4.299183
12	130	SEQ ID NO: 7728	0.00 %	4.138344
13	84	SEQ ID NO: 7729	0.00 %	3.42792
14	27	SEQ ID NO: 7730	0.00 %	3.383484
15	2	SEQ ID NO: 7731	0.00 %	3.381
16	62	SEQ ID NO: 7732	0.00 %	3.251556
17	23	SEQ ID NO: 7733	0.00 %	2.9542005
18	99	SEQ ID NO: 7734	0.00 %	1.982232
19	33	SEQ ID NO: 7735	0.00 %	1.86921
20	111	SEQ ID NO: 7736	0.00 %	1.76402985

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	5	SEQ ID NO: 7737	0.00 %	159.9696
2	25	SEQ ID NO: 7738	0.00 %	69.552
3	80	SEQ ID NO: 7739	0.00 %	36.5148
4	107	SEQ ID NO: 7740	0.00 %	21.3624

5	148	SEQ ID NO: 7741	0.00 %	17.73576
6	61	SEQ ID NO: 7742	0.00 %	13.9104
7	147	SEQ ID NO: 7743	0.00 %	11.304684
8	53	SEQ ID NO: 7744	0.00 %	8.230458
9	17	SEQ ID NO: 7745	0.00 %	7.3086111
10	110	SEQ ID NO: 7746	0.00 %	6.174104475
11	9	SEQ ID NO: 7747	0.00 %	6.0858
12	99	SEQ ID NO: 7748	0.00 %	5.6823984
13	2	SEQ ID NO: 7749	0.00 %	3.188283
14	41	SEQ ID NO: 7750	0.00 %	2.206413
15	135	SEQ ID NO: 7751	0.00 %	2.076624
16	76	SEQ ID NO: 7752	0.00 %	2.005692
17	23	SEQ ID NO: 7753	0.00 %	1.798209
18	40	SEQ ID NO: 7754	0.00 %	1.68996456
19	39	SEQ ID NO: 7755	0.00 %	1.516482
20	118	SEQ ID NO: 7756	0.00 %	1.2683304

HLA A 1101 - 9 mers

Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	91	SEQ ID NO: 7757	2.77 %	1

HLA A 1101 - 10 mers

Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	101	SEQ ID NO: 7758	33.33 %	12
2	71	SEQ ID NO: 7759	2.77 %	1
3	90	SEQ ID NO: 7760	1.66 %	0.6

HLA B7 - 9 mers

Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	49	SEQ ID NO: 7761	2.22 %	120
2	9	SEQ ID NO: 7762	1.11 %	60
3	73	SEQ ID NO: 7763	0.66 %	36
4	33	SEQ ID NO: 7764	0.37 %	20
5	137	SEQ ID NO: 7765	0.37 %	20
6	141	SEQ ID NO: 7766	0.37 %	20
7	77	SEQ ID NO: 7767	0.22 %	12

8	112	SEQ ID NO: 7768	0.22 %	12
9	143	SEQ ID NO: 7769	0.22 %	12
10	81	SEQ ID NO: 7770	0.14 %	8
11	13	SEQ ID NO: 7771	0.09 %	5
12	69	SEQ ID NO: 7772	0.09 %	5
13	18	SEQ ID NO: 7773	0.07 %	4
14	32	SEQ ID NO: 7774	0.07 %	4
15	54	SEQ ID NO: 7775	0.07 %	4
16	80	SEQ ID NO: 7776	0.07 %	4
17	92	SEQ ID NO: 7777	0.07 %	4
18	108	SEQ ID NO: 7778	0.07 %	4
19	111	SEQ ID NO: 7779	0.07 %	4
20	123	SEQ ID NO: 7780	0.07 %	4

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	99	SEQ ID NO: 7781	0.74 %	40
2	17	SEQ ID NO: 7782	0.37 %	20
3	8	SEQ ID NO: 7783	0.22 %	12
4	72	SEQ ID NO: 7784	0.22 %	12
5	91	SEQ ID NO: 7785	0.22 %	12
6	127	SEQ ID NO: 7786	0.11 %	6
7	31	SEQ ID NO: 7787	0.07 %	4
8	32	SEQ ID NO: 7788	0.07 %	4
9	53	SEQ ID NO: 7789	0.07 %	4
10	76	SEQ ID NO: 7790	0.07 %	4
11	107	SEQ ID NO: 7791	0.07 %	4
12	110	SEQ ID NO: 7792	0.07 %	4
13	111	SEQ ID NO: 7793	0.07 %	4
14	140	SEQ ID NO: 7794	0.07 %	4
15	9	SEQ ID NO: 7795	0.05 %	3
16	19	SEQ ID NO: 7796	0.05 %	3
17	33	SEQ ID NO: 7797	0.03 %	2
18	93	SEQ ID NO: 7798	0.03 %	2
19	102	SEQ ID NO: 7799	0.03 %	2
20	129	SEQ ID NO: 7800	0.02 %	1.5

Table 15: Epitopes for SEQ ID NO: 6041

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	1818	SEQ ID NO: 7801	1.6 %	90
2	373	SEQ ID NO: 7802	1.33 %	75
3	681	SEQ ID NO: 7803	1.33 %	75
4	74	SEQ ID NO: 7804	0.88 %	50
5	786	SEQ ID NO: 7805	0.88 %	50
6	1495	SEQ ID NO: 7806	0.88 %	50
7	88	SEQ ID NO: 7807	0.8 %	45
8	357	SEQ ID NO: 7808	0.8 %	45
9	1271	SEQ ID NO: 7809	0.8 %	45
10	1799	SEQ ID NO: 7810	0.8 %	45
11	1393	SEQ ID NO: 7811	0.48 %	27
12	386	SEQ ID NO: 7812	0.44 %	25
13	2304	SEQ ID NO: 7813	0.44 %	25
14	198	SEQ ID NO: 7814	0.4 %	22.5
15	840	SEQ ID NO: 7815	0.4 %	22.5
16	2359	SEQ ID NO: 7816	0.4 %	22.5
17	1194	SEQ ID NO: 7817	0.32 %	18
18	1546	SEQ ID NO: 7818	0.32 %	18
19	2200	SEQ ID NO: 7819	0.22 %	12.5
20	996	SEQ ID NO: 7820	0.2 %	11.25

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	995	SEQ ID NO: 7821	10 %	562.5
2	1303	SEQ ID NO: 7822	2.22 %	125
3	1582	SEQ ID NO: 7823	2 %	112.5
4	1456	SEQ ID NO: 7824	1.6 %	90
5	772	SEQ ID NO: 7825	1.11 %	62.5
6	181	SEQ ID NO: 7826	0.88 %	50
7	632	SEQ ID NO: 7827	0.88 %	50
8	2281	SEQ ID NO: 7828	0.88 %	50
9	1586	SEQ ID NO: 7829	0.8 %	45
10	2109	SEQ ID NO: 7830	0.8 %	45
11	745	SEQ ID NO: 7831	0.55 %	31.25

12	1916	SEQ ID NO: 7832	0.53 %	30
13	966	SEQ ID NO: 7833	0.44 %	25
14	1387	SEQ ID NO: 7834	0.44 %	25
15	2263	SEQ ID NO: 7835	0.44 %	25
16	2457	SEQ ID NO: 7836	0.26 %	15
17	1057	SEQ ID NO: 7837	0.22 %	12.5
18	2562	SEQ ID NO: 7838	0.22 %	12.5
19	74	SEQ ID NO: 7839	0.17 %	10
20	298	SEQ ID NO: 7840	0.17 %	10

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	536	SEQ ID NO: 7841	3.33 %	405
2	986	SEQ ID NO: 7842	2.46 %	300
3	805	SEQ ID NO: 7843	1.64 %	200
4	2345	SEQ ID NO: 7844	1.48 %	180
5	2481	SEQ ID NO: 7845	0.55 %	67.5
6	204	SEQ ID NO: 7846	0.49 %	60
7	895	SEQ ID NO: 7847	0.44 %	54
8	1512	SEQ ID NO: 7848	0.44 %	54
9	2491	SEQ ID NO: 7849	0.37 %	45
10	436	SEQ ID NO: 7850	0.32 %	40
11	917	SEQ ID NO: 7851	0.32 %	40
12	1176	SEQ ID NO: 7852	0.32 %	40
13	1517	SEQ ID NO: 7853	0.29 %	36
14	466	SEQ ID NO: 7854	0.24 %	30
15	1784	SEQ ID NO: 7855	0.24 %	30
16	2039	SEQ ID NO: 7856	0.24 %	30
17	2124	SEQ ID NO: 7857	0.24 %	30
18	1049	SEQ ID NO: 7858	0.22 %	27
19	2200	SEQ ID NO: 7859	0.22 %	27
20	2598	SEQ ID NO: 7860	0.22 %	27

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	392	SEQ ID NO: 7861	2.46 %	300
2	2230	SEQ ID NO: 7862	1.48 %	180

3	590	SEQ ID NO: 7863	1.11 %	135
4	697	SEQ ID NO: 7864	1.11 %	135
5	919	SEQ ID NO: 7865	0.74 %	90
6	1354	SEQ ID NO: 7866	0.74 %	90
7	1430	SEQ ID NO: 7867	0.74 %	90
8	2534	SEQ ID NO: 7868	0.74 %	90
9	202	SEQ ID NO: 7869	0.49 %	60
10	488	SEQ ID NO: 7870	0.49 %	60
11	922	SEQ ID NO: 7871	0.49 %	60
12	1735	SEQ ID NO: 7872	0.49 %	60
13	2281	SEQ ID NO: 7873	0.49 %	60
14	1894	SEQ ID NO: 7874	0.44 %	54
15	2552	SEQ ID NO: 7875	0.44 %	54
16	555	SEQ ID NO: 7876	0.37 %	45
17	1134	SEQ ID NO: 7877	0.37 %	45
18	1149	SEQ ID NO: 7878	0.29 %	36
19	283	SEQ ID NO: 7879	0.24 %	30
20	917	SEQ ID NO: 7880	0.24 %	30

HLA A24 - 9 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	2375	SEQ ID NO: 7881	36.07 %	576
2	1751	SEQ ID NO: 7882	28.93 %	462
3	195	SEQ ID NO: 7883	25.05 %	400
4	2306	SEQ ID NO: 7884	21.04 %	336
5	806	SEQ ID NO: 7885	20.66 %	330
6	1252	SEQ ID NO: 7886	18.78 %	300
7	160	SEQ ID NO: 7887	15.03 %	240
8	517	SEQ ID NO: 7888	15.03 %	240
9	375	SEQ ID NO: 7889	12.52 %	200
10	1275	SEQ ID NO: 7890	12.52 %	200
11	2175	SEQ ID NO: 7891	12.52 %	200
12	2207	SEQ ID NO: 7892	12.52 %	200
13	2343	SEQ ID NO: 7893	12.52 %	200
14	443	SEQ ID NO: 7894	11.27 %	180
15	668	SEQ ID NO: 7895	7.51 %	120
16	1825	SEQ ID NO: 7896	6.88 %	110
17	1690	SEQ ID NO: 7897	4.69 %	75

18	159	SEQ ID NO: 7898	3.75 %	60
19	2550	SEQ ID NO: 7899	3.75 %	60
20	1949	SEQ ID NO: 7900	3.38 %	54

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	641	SEQ ID NO: 7901	45.09 %	720
2	809	SEQ ID NO: 7902	24.80 %	396
3	1209	SEQ ID NO: 7903	22.54 %	360
4	216	SEQ ID NO: 7904	18.03 %	288
5	159	SEQ ID NO: 7905	15.03 %	240
6	528	SEQ ID NO: 7906	15.03 %	240
7	799	SEQ ID NO: 7907	15.03 %	240
8	1436	SEQ ID NO: 7908	15.03 %	240
9	2219	SEQ ID NO: 7909	15.03 %	240
10	1065	SEQ ID NO: 7910	13.77 %	220
11	1953	SEQ ID NO: 7911	13.15 %	210
12	1966	SEQ ID NO: 7912	12.52 %	200
13	2600	SEQ ID NO: 7913	12.52 %	200
14	71	SEQ ID NO: 7914	9.39 %	150
15	380	SEQ ID NO: 7915	9.39 %	150
16	1989	SEQ ID NO: 7916	9.39 %	150
17	342	SEQ ID NO: 7917	8.76 %	140
18	1071	SEQ ID NO: 7918	8.76 %	140
19	2570	SEQ ID NO: 7919	6.88 %	110
20	2550	SEQ ID NO: 7920	6.26 %	100

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	1632	SEQ ID NO: 7921	0.09 %	3607.31448
2	1640	SEQ ID NO: 7922	0.04 %	1748.2560912
3	1776	SEQ ID NO: 7923	0.03 %	1492.58592
4	2512	SEQ ID NO: 7924	0.03 %	1434.16845
5	1073	SEQ ID NO: 7925	0.03 %	1338.876
6	230	SEQ ID NO: 7926	0.01 %	685.78272
7	1001	SEQ ID NO: 7927	0.01 %	559.8936
8	716	SEQ ID NO: 7928	0.01 %	558.27486

9	2280	SEQ ID NO: 7929	0.01 %	511.19781048
10	590	SEQ ID NO: 7930	0.01 %	469.6692
11	664	SEQ ID NO: 7931	0.01 %	442.076389524
12	1094	SEQ ID NO: 7932	0.00 %	382.536
13	1735	SEQ ID NO: 7933	0.00 %	382.536
14	1625	SEQ ID NO: 7934	0.00 %	342.4606344
15	1974	SEQ ID NO: 7935	0.00 %	336.885048
16	2382	SEQ ID NO: 7936	0.00 %	319.9392
17	2417	SEQ ID NO: 7937	0.00 %	319.9392
18	744	SEQ ID NO: 7938	0.00 %	256.416670125
19	108	SEQ ID NO: 7939	0.00 %	232.52724
20	390	SEQ ID NO: 7940	0.00 %	228.0411084

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	2511	SEQ ID NO: 7941	0.38 %	15126.90795
2	1608	SEQ ID NO: 7942	0.05 %	2049.4656
3	2572	SEQ ID NO: 7943	0.04 %	1879.5921264
4	255	SEQ ID NO: 7944	0.03 %	1566.6522795
5	895	SEQ ID NO: 7945	0.03 %	1338.876
6	1171	SEQ ID NO: 7946	0.02 %	1107.960876
7	1691	SEQ ID NO: 7947	0.01 %	782.95521024
8	20	SEQ ID NO: 7948	0.01 %	549.9372312
9	1632	SEQ ID NO: 7949	0.01 %	479.041993296
10	2280	SEQ ID NO: 7950	0.01 %	472.418344576987
11	1963	SEQ ID NO: 7951	0.00 %	358.73928
12	1955	SEQ ID NO: 7952	0.00 %	331.093464
13	741	SEQ ID NO: 7953	0.00 %	318.652488
14	523	SEQ ID NO: 7954	0.00 %	278.7876
15	1073	SEQ ID NO: 7955	0.00 %	266.6988828
16	2489	SEQ ID NO: 7956	0.00 %	243.432
17	777	SEQ ID NO: 7957	0.00 %	218.5730664
18	1737	SEQ ID NO: 7958	0.00 %	218.0785572
19	589	SEQ ID NO: 7959	0.00 %	210.538251
20	229	SEQ ID NO: 7960	0.00 %	205.230564

HLA A 1101 - 9 mers	
Maximum possible score using this molecule type	36

Rank	Start position	Sequence	% of max. score	Score
1	2337	SEQ ID NO: 7961	33.33 %	12
2	2156	SEQ ID NO: 7962	25 %	9
3	492	SEQ ID NO: 7963	20 %	7.2
4	18	SEQ ID NO: 7964	16.66 %	6
5	332	SEQ ID NO: 7965	16.66 %	6
6	415	SEQ ID NO: 7966	16.66 %	6
7	2479	SEQ ID NO: 7967	16.66 %	6
8	1495	SEQ ID NO: 7968	11.11 %	4
9	2035	SEQ ID NO: 7969	11.11 %	4
10	1349	SEQ ID NO: 7970	10 %	3.6
11	1194	SEQ ID NO: 7971	8.33 %	3
12	1648	SEQ ID NO: 7972	8.33 %	3
13	96	SEQ ID NO: 7973	6.66 %	2.4
14	764	SEQ ID NO: 7974	6.66 %	2.4
15	986	SEQ ID NO: 7975	6.66 %	2.4
16	2345	SEQ ID NO: 7976	6.66 %	2.4
17	698	SEQ ID NO: 7977	5.55 %	2
18	1355	SEQ ID NO: 7978	5.55 %	2
19	1987	SEQ ID NO: 7979	5.55 %	2
20	2085	SEQ ID NO: 7980	5.55 %	2

HLA A 1101 - 10 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	2083	SEQ ID NO: 7981	33.33 %	12
2	2123	SEQ ID NO: 7982	25 %	9
3	2147	SEQ ID NO: 7983	16.66 %	6
4	331	SEQ ID NO: 7984	12.5 %	4.5
5	1035	SEQ ID NO: 7985	11.11 %	4
6	1064	SEQ ID NO: 7986	11.11 %	4
7	2154	SEQ ID NO: 7987	11.11 %	4
8	1048	SEQ ID NO: 7988	7.5 %	2.7
9	202	SEQ ID NO: 7989	6.66 %	2.4
10	721	SEQ ID NO: 7990	6.66 %	2.4
11	2109	SEQ ID NO: 7991	6.66 %	2.4
12	2230	SEQ ID NO: 7992	6.66 %	2.4
13	1306	SEQ ID NO: 7993	5.55 %	2
14	1622	SEQ ID NO: 7994	5.55 %	2

15	1772	SEQ ID NO: 7995	5.55 %	2
16	1796	SEQ ID NO: 7996	5.55 %	2
17	186	SEQ ID NO: 7997	5 %	1.8
18	414	SEQ ID NO: 7998	5 %	1.8
19	697	SEQ ID NO: 7999	5 %	1.8
20	1175	SEQ ID NO: 8000	5 %	1.8

HLA B7 - 9 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	1447	SEQ ID NO: 8001	14.81 %	800
2	642	SEQ ID NO: 8002	3.70 %	200
3	34	SEQ ID NO: 8003	2.22 %	120
4	186	SEQ ID NO: 8004	1.48 %	80
5	244	SEQ ID NO: 8005	1.48 %	80
6	459	SEQ ID NO: 8006	1.48 %	80
7	1475	SEQ ID NO: 8007	1.48 %	80
8	1867	SEQ ID NO: 8008	1.48 %	80
9	2032	SEQ ID NO: 8009	1.48 %	80
10	2047	SEQ ID NO: 8010	1.48 %	80
11	2335	SEQ ID NO: 8011	1.48 %	80
12	622	SEQ ID NO: 8012	1.11 %	60
13	1375	SEQ ID NO: 8013	1.11 %	60
14	1617	SEQ ID NO: 8014	0.92 %	50
15	1023	SEQ ID NO: 8015	0.83 %	45
16	286	SEQ ID NO: 8016	0.74 %	40
17	490	SEQ ID NO: 8017	0.74 %	40
18	810	SEQ ID NO: 8018	0.74 %	40
19	1420	SEQ ID NO: 8019	0.74 %	40
20	1854	SEQ ID NO: 8020	0.74 %	40

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	1617	SEQ ID NO: 8021	3.70 %	200
2	752	SEQ ID NO: 8022	2.22 %	120
3	1552	SEQ ID NO: 8023	2.22 %	120
4	154	SEQ ID NO: 8024	1.48 %	80
5	165	SEQ ID NO: 8025	1.48 %	80

6	383	SEQ ID NO: 8026	1.48 %	80
7	1501	SEQ ID NO: 8027	1.48 %	80
8	2093	SEQ ID NO: 8028	1.48 %	80
9	2564	SEQ ID NO: 8029	1.48 %	80
10	622	SEQ ID NO: 8030	1.11 %	60
11	1086	SEQ ID NO: 8031	1.11 %	60
12	1262	SEQ ID NO: 8032	1.11 %	60
13	1556	SEQ ID NO: 8033	1.11 %	60
14	845	SEQ ID NO: 8034	1 %	54
15	286	SEQ ID NO: 8035	0.74 %	40
16	490	SEQ ID NO: 8036	0.74 %	40
17	552	SEQ ID NO: 8037	0.74 %	40
18	1858	SEQ ID NO: 8038	0.74 %	40
19	2107	SEQ ID NO: 8039	0.74 %	40
20	2582	SEQ ID NO: 8040	0.74 %	40

Table 16: Epitopes for SEQ ID NO: 6042

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	846	SEQ ID NO: 8041	2.22 %	125
2	798	SEQ ID NO: 8042	1.6 %	90
3	787	SEQ ID NO: 8043	0.88 %	50
4	1178	SEQ ID NO: 8044	0.88 %	50
5	637	SEQ ID NO: 8045	0.8 %	45
6	557	SEQ ID NO: 8046	0.44 %	25
7	1020	SEQ ID NO: 8047	0.44 %	25
8	282	SEQ ID NO: 8048	0.32 %	18
9	1241	SEQ ID NO: 8049	0.24 %	13.5
10	466	SEQ ID NO: 8050	0.22 %	12.5
11	727	SEQ ID NO: 8051	0.2 %	11.25
12	706	SEQ ID NO: 8052	0.17 %	10
13	324	SEQ ID NO: 8053	0.16 %	9
14	752	SEQ ID NO: 8054	0.16 %	9
15	54	SEQ ID NO: 8055	0.13 %	7.5
16	554	SEQ ID NO: 8056	0.13 %	7.5
17	590	SEQ ID NO: 8057	0.12 %	6.75

18	569	SEQ ID NO: 8058	0.08 %	5
19	613	SEQ ID NO: 8059	0.08 %	5
20	90	SEQ ID NO: 8060	0.08 %	4.5

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	1241	SEQ ID NO: 8061	4.8 %	270
2	967	SEQ ID NO: 8062	0.8 %	45
3	1010	SEQ ID NO: 8063	0.48 %	27
4	426	SEQ ID NO: 8064	0.44 %	25
5	809	SEQ ID NO: 8065	0.44 %	25
6	1178	SEQ ID NO: 8066	0.44 %	25
7	787	SEQ ID NO: 8067	0.22 %	12.5
8	958	SEQ ID NO: 8068	0.22 %	12.5
9	727	SEQ ID NO: 8069	0.2 %	11.25
10	610	SEQ ID NO: 8070	0.17 %	10
11	12	SEQ ID NO: 8071	0.13 %	7.5
12	1181	SEQ ID NO: 8072	0.12 %	6.75
13	373	SEQ ID NO: 8073	0.11 %	6.25
14	602	SEQ ID NO: 8074	0.11 %	6.25
15	20	SEQ ID NO: 8075	0.04 %	2.5
16	32	SEQ ID NO: 8076	0.04 %	2.5
17	53	SEQ ID NO: 8077	0.04 %	2.5
18	400	SEQ ID NO: 8078	0.04 %	2.5
19	557	SEQ ID NO: 8079	0.04 %	2.5
20	667	SEQ ID NO: 8080	0.04 %	2.5

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	768	SEQ ID NO: 8081	0.82 %	100
2	808	SEQ ID NO: 8082	0.49 %	60
3	85	SEQ ID NO: 8083	0.24 %	30
4	663	SEQ ID NO: 8084	0.24 %	30
5	1245	SEQ ID NO: 8085	0.14 %	18
6	288	SEQ ID NO: 8086	0.09 %	12
7	50	SEQ ID NO: 8087	0.08 %	10
8	320	SEQ ID NO: 8088	0.07 %	9

9	402	SEQ ID NO: 8089	0.07 %	9
10	798	SEQ ID NO: 8090	0.07 %	9
11	902	SEQ ID NO: 8091	0.06 %	8.1
12	364	SEQ ID NO: 8092	0.05 %	6.75
13	297	SEQ ID NO: 8093	0.04 %	6
14	992	SEQ ID NO: 8094	0.04 %	6
15	38	SEQ ID NO: 8095	0.03 %	4.5
16	249	SEQ ID NO: 8096	0.03 %	4.5
17	706	SEQ ID NO: 8097	0.03 %	4.05
18	1204	SEQ ID NO: 8098	0.03 %	4.05
19	1178	SEQ ID NO: 8099	0.03 %	4
20	343	SEQ ID NO: 8100	0.02 %	3.6

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	255	SEQ ID NO: 8101	1.48 %	180
2	180	SEQ ID NO: 8102	0.55 %	67.5
3	768	SEQ ID NO: 8103	0.49 %	60
4	1177	SEQ ID NO: 8104	0.49 %	60
5	380	SEQ ID NO: 8105	0.24 %	30
6	100	SEQ ID NO: 8106	0.18 %	22.5
7	786	SEQ ID NO: 8107	0.16 %	20
8	1217	SEQ ID NO: 8108	0.16 %	20
9	207	SEQ ID NO: 8109	0.14 %	18
10	1183	SEQ ID NO: 8110	0.14 %	18
11	38	SEQ ID NO: 8111	0.09 %	12
12	52	SEQ ID NO: 8112	0.09 %	12
13	8	SEQ ID NO: 8113	0.06 %	8
14	679	SEQ ID NO: 8114	0.06 %	8
15	73	SEQ ID NO: 8115	0.05 %	6.75
16	1204	SEQ ID NO: 8116	0.05 %	6.075
17	50	SEQ ID NO: 8117	0.04 %	6
18	774	SEQ ID NO: 8118	0.04 %	6
19	845	SEQ ID NO: 8119	0.04 %	6
20	214	SEQ ID NO: 8120	0.04 %	5.4

HLA A24 - 9 mers	
Maximum possible score using this molecule type	1596.672

Rank	Start position	Sequence	% of max. score	Score
1	1118	SEQ ID NO: 8121	19.84 %	316.8
2	51	SEQ ID NO: 8122	18.78 %	300
3	161	SEQ ID NO: 8123	18.78 %	300
4	434	SEQ ID NO: 8124	18.78 %	300
5	365	SEQ ID NO: 8125	13.77 %	220
6	736	SEQ ID NO: 8126	12.52 %	200
7	620	SEQ ID NO: 8127	7.51 %	120
8	1068	SEQ ID NO: 8128	7.51 %	120
9	817	SEQ ID NO: 8129	3.75 %	60
10	336	SEQ ID NO: 8130	3.44 %	55
11	687	SEQ ID NO: 8131	3.13 %	50
12	254	SEQ ID NO: 8132	2.34 %	37.5
13	627	SEQ ID NO: 8133	1.87 %	30
14	950	SEQ ID NO: 8134	1.75 %	28
15	28	SEQ ID NO: 8135	1.56 %	25
16	408	SEQ ID NO: 8136	1.56 %	25
17	159	SEQ ID NO: 8137	1.31 %	21
18	1166	SEQ ID NO: 8138	1.26 %	20.16
19	45	SEQ ID NO: 8139	1.25 %	20
20	185	SEQ ID NO: 8140	1.25 %	20

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	438	SEQ ID NO: 8141	27.55 %	440
2	489	SEQ ID NO: 8142	22.54 %	360
3	254	SEQ ID NO: 8143	18.78 %	300
4	354	SEQ ID NO: 8144	11.27 %	180
5	406	SEQ ID NO: 8145	11.27 %	180
6	1047	SEQ ID NO: 8146	11.27 %	180
7	473	SEQ ID NO: 8147	7.51 %	120
8	350	SEQ ID NO: 8148	6.26 %	100
9	769	SEQ ID NO: 8149	6.26 %	100
10	193	SEQ ID NO: 8150	5.63 %	90
11	479	SEQ ID NO: 8151	3.13 %	50
12	0	SEQ ID NO: 8152	2.70 %	43.2
13	813	SEQ ID NO: 8153	1.87 %	30
14	739	SEQ ID NO: 8154	1.50 %	24

15	782	SEQ ID NO: 8155	1.50 %	24
16	1186	SEQ ID NO: 8156	1.31 %	21
17	910	SEQ ID NO: 8157	1.05 %	16.8
18	128	SEQ ID NO: 8158	0.93 %	15
19	183	SEQ ID NO: 8159	0.93 %	15
20	1069	SEQ ID NO: 8160	0.93 %	15

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	1041	SEQ ID NO: 8161	0.01 %	484.2379773
2	981	SEQ ID NO: 8162	0.00 %	382.536
3	957	SEQ ID NO: 8163	0.00 %	342.4606344
4	896	SEQ ID NO: 8164	0.00 %	232.6931712
5	1173	SEQ ID NO: 8165	0.00 %	201.447432
6	733	SEQ ID NO: 8166	0.00 %	171.86796
7	410	SEQ ID NO: 8167	0.00 %	135.45252
8	786	SEQ ID NO: 8168	0.00 %	119.463012
9	150	SEQ ID NO: 8169	0.00 %	102.17550222
10	1	SEQ ID NO: 8170	0.00 %	94.98737754
11	595	SEQ ID NO: 8171	0.00 %	93.239424
12	1095	SEQ ID NO: 8172	0.00 %	89.41779
13	1166	SEQ ID NO: 8173	0.00 %	87.58584
14	845	SEQ ID NO: 8174	0.00 %	79.642008
15	734	SEQ ID NO: 8175	0.00 %	73.47672
16	802	SEQ ID NO: 8176	0.00 %	71.872056
17	1213	SEQ ID NO: 8177	0.00 %	71.872056
18	105	SEQ ID NO: 8178	0.00 %	50.232
19	939	SEQ ID NO: 8179	0.00 %	49.13352
20	130	SEQ ID NO: 8180	0.00 %	48.732354

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	372	SEQ ID NO: 8181	0.04 %	1896.33528
2	410	SEQ ID NO: 8182	0.02 %	1134.00849744
3	162	SEQ ID NO: 8183	0.01 %	685.3897512
4	1076	SEQ ID NO: 8184	0.01 %	640.90320525
5	1196	SEQ ID NO: 8185	0.01 %	623.742666372

6	353	SEQ ID NO: 8186	0.01 %	446.7384576
7	50	SEQ ID NO: 8187	0.00 %	375.97824
8	733	SEQ ID NO: 8188	0.00 %	271.863864
9	130	SEQ ID NO: 8189	0.00 %	235.6873848
10	415	SEQ ID NO: 8190	0.00 %	185.679
11	297	SEQ ID NO: 8191	0.00 %	177.496704
12	1	SEQ ID NO: 8192	0.00 %	152.42160582
13	56	SEQ ID NO: 8193	0.00 %	110.013876
14	732	SEQ ID NO: 8194	0.00 %	101.0988
15	6	SEQ ID NO: 8195	0.00 %	98.26704
16	261	SEQ ID NO: 8196	0.00 %	91.60164
17	1040	SEQ ID NO: 8197	0.00 %	76.98537
18	928	SEQ ID NO: 8198	0.00 %	71.2908
19	1188	SEQ ID NO: 8199	0.00 %	69.81282
20	1094	SEQ ID NO: 8200	0.00 %	52.5987

HLA A 1101 - 9 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	402	SEQ ID NO: 8201	25 %	9
2	902	SEQ ID NO: 8202	22.5 %	8.1
3	288	SEQ ID NO: 8203	11.11 %	4
4	85	SEQ ID NO: 8204	6.66 %	2.4
5	706	SEQ ID NO: 8205	6.66 %	2.4
6	456	SEQ ID NO: 8206	5.55 %	2
7	920	SEQ ID NO: 8207	5.55 %	2
8	535	SEQ ID NO: 8208	5 %	1.8
9	364	SEQ ID NO: 8209	3.33 %	1.2
10	438	SEQ ID NO: 8210	3.33 %	1.2
11	798	SEQ ID NO: 8211	3.33 %	1.2
12	808	SEQ ID NO: 8212	3.33 %	1.2
13	937	SEQ ID NO: 8213	3.33 %	1.2
14	956	SEQ ID NO: 8214	3.33 %	1.2
15	557	SEQ ID NO: 8215	2.77 %	1
16	1218	SEQ ID NO: 8216	2.77 %	1
17	784	SEQ ID NO: 8217	2.5 %	0.9
18	249	SEQ ID NO: 8218	2.22 %	0.8
19	768	SEQ ID NO: 8219	2.22 %	0.8
20	1178	SEQ ID NO: 8220	2.22 %	0.8

HLA A 1101 - 10 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	38	SEQ ID NO: 8221	13.33 %	4.8
2	807	SEQ ID NO: 8222	12.5 %	4.5
3	100	SEQ ID NO: 8223	11.11 %	4
4	380	SEQ ID NO: 8224	11.11 %	4
5	767	SEQ ID NO: 8225	10 %	3.6
6	533	SEQ ID NO: 8226	8.33 %	3
7	967	SEQ ID NO: 8227	6.66 %	2.4
8	919	SEQ ID NO: 8228	5.55 %	2
9	305	SEQ ID NO: 8229	5 %	1.8
10	211	SEQ ID NO: 8230	3.33 %	1.2
11	511	SEQ ID NO: 8231	3.33 %	1.2
12	1177	SEQ ID NO: 8232	3.33 %	1.2
13	429	SEQ ID NO: 8233	2.77 %	1
14	758	SEQ ID NO: 8234	2.77 %	1
15	797	SEQ ID NO: 8235	2.5 %	0.9
16	255	SEQ ID NO: 8236	2.22 %	0.8
17	986	SEQ ID NO: 8237	2.22 %	0.8
18	1157	SEQ ID NO: 8238	2.22 %	0.8
19	170	SEQ ID NO: 8239	1.66 %	0.6
20	893	SEQ ID NO: 8240	1.66 %	0.6

HLA B7 - 9 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	200	SEQ ID NO: 8241	1.48 %	80
2	1243	SEQ ID NO: 8242	1.48 %	80
3	123	SEQ ID NO: 8243	0.74 %	40
4	248	SEQ ID NO: 8244	0.66 %	36
5	1036	SEQ ID NO: 8245	0.66 %	36
6	494	SEQ ID NO: 8246	0.37 %	20
7	495	SEQ ID NO: 8247	0.37 %	20
8	523	SEQ ID NO: 8248	0.37 %	20
9	842	SEQ ID NO: 8249	0.37 %	20
10	932	SEQ ID NO: 8250	0.37 %	20
11	274	SEQ ID NO: 8251	0.33 %	18

12	588	SEQ ID NO: 8252	0.22 %	12
13	656	SEQ ID NO: 8253	0.22 %	12
14	657	SEQ ID NO: 8254	0.22 %	12
15	767	SEQ ID NO: 8255	0.22 %	12
16	911	SEQ ID NO: 8256	0.22 %	12
17	939	SEQ ID NO: 8257	0.22 %	12
18	1007	SEQ ID NO: 8258	0.22 %	12
19	1170	SEQ ID NO: 8259	0.22 %	12
20	1206	SEQ ID NO: 8260	0.22 %	12

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	505	SEQ ID NO: 8261	4.44 %	240
2	312	SEQ ID NO: 8262	3.70 %	200
3	141	SEQ ID NO: 8263	1.11 %	60
4	1006	SEQ ID NO: 8264	0.66 %	36
5	411	SEQ ID NO: 8265	0.44 %	24
6	122	SEQ ID NO: 8266	0.37 %	20
7	134	SEQ ID NO: 8267	0.37 %	20
8	184	SEQ ID NO: 8268	0.37 %	20
9	367	SEQ ID NO: 8269	0.37 %	20
10	402	SEQ ID NO: 8270	0.37 %	20
11	494	SEQ ID NO: 8271	0.37 %	20
12	560	SEQ ID NO: 8272	0.37 %	20
13	626	SEQ ID NO: 8273	0.37 %	20
14	931	SEQ ID NO: 8274	0.37 %	20
15	956	SEQ ID NO: 8275	0.37 %	20
16	1117	SEQ ID NO: 8276	0.37 %	20
17	1169	SEQ ID NO: 8277	0.37 %	20
18	1196	SEQ ID NO: 8278	0.37 %	20
19	247	SEQ ID NO: 8279	0.22 %	12
20	273	SEQ ID NO: 8280	0.22 %	12

Table 17: Epitopes for SEQ ID NO: 6043

HLA A1 - 9 mers	
Maximum possible score using this molecule type	5625

Rank	Start position	Sequence	% of max. score	Score
1	168	SEQ ID NO: 8281	0.2 %	11.25
2	212	SEQ ID NO: 8282	0.08 %	4.5
3	223	SEQ ID NO: 8283	0.08 %	4.5
4	104	SEQ ID NO: 8284	0.04 %	2.5
5	170	SEQ ID NO: 8285	0.04 %	2.5
6	99	SEQ ID NO: 8286	0.04 %	2.25
7	188	SEQ ID NO: 8287	0.02 %	1.35
8	180	SEQ ID NO: 8288	0.02 %	1.25
9	219	SEQ ID NO: 8289	0.02 %	1.25
10	18	SEQ ID NO: 8290	0.01 %	1
11	226	SEQ ID NO: 8291	0.01 %	1
12	98	SEQ ID NO: 8292	0.01 %	0.625
13	151	SEQ ID NO: 8293	0.01 %	0.625
14	10	SEQ ID NO: 8294	0.01 %	0.6
15	13	SEQ ID NO: 8295	0.00 %	0.5
16	32	SEQ ID NO: 8296	0.00 %	0.5
17	70	SEQ ID NO: 8297	0.00 %	0.5
18	78	SEQ ID NO: 8298	0.00 %	0.5
19	82	SEQ ID NO: 8299	0.00 %	0.5
20	145	SEQ ID NO: 8300	0.00 %	0.5

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	99	SEQ ID NO: 8301	0.8 %	45
2	223	SEQ ID NO: 8302	0.8 %	45
3	188	SEQ ID NO: 8303	0.48 %	27
4	206	SEQ ID NO: 8304	0.2 %	11.25
5	253	SEQ ID NO: 8305	0.17 %	10
6	174	SEQ ID NO: 8306	0.13 %	7.5
7	97	SEQ ID NO: 8307	0.04 %	2.5
8	257	SEQ ID NO: 8308	0.04 %	2.5
9	179	SEQ ID NO: 8309	0.04 %	2.25
10	162	SEQ ID NO: 8310	0.02 %	1.25
11	196	SEQ ID NO: 8311	0.02 %	1.25
12	219	SEQ ID NO: 8312	0.02 %	1.25
13	18	SEQ ID NO: 8313	0.01 %	1
14	246	SEQ ID NO: 8314	0.01 %	1

15	38	SEQ ID NO: 8315	0.01 %	0.75
16	33	SEQ ID NO: 8316	0.00 %	0.5
17	69	SEQ ID NO: 8317	0.00 %	0.5
18	81	SEQ ID NO: 8318	0.00 %	0.5
19	104	SEQ ID NO: 8319	0.00 %	0.5
20	116	SEQ ID NO: 8320	0.00 %	0.5

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	104	SEQ ID NO: 8321	0.98 %	120
2	123	SEQ ID NO: 8322	0.74 %	90
3	82	SEQ ID NO: 8323	0.44 %	54
4	106	SEQ ID NO: 8324	0.11 %	13.5
5	99	SEQ ID NO: 8325	0.08 %	10.8
6	127	SEQ ID NO: 8326	0.08 %	10
7	71	SEQ ID NO: 8327	0.07 %	9
8	1	SEQ ID NO: 8328	0.06 %	8.1
9	113	SEQ ID NO: 8329	0.04 %	6
10	84	SEQ ID NO: 8330	0.03 %	4.5
11	109	SEQ ID NO: 8331	0.03 %	4.05
12	58	SEQ ID NO: 8332	0.02 %	3
13	138	SEQ ID NO: 8333	0.02 %	3
14	44	SEQ ID NO: 8334	0.02 %	2.7
15	81	SEQ ID NO: 8335	0.02 %	2.7
16	226	SEQ ID NO: 8336	0.02 %	2.7
17	184	SEQ ID NO: 8337	0.01 %	1.8
18	102	SEQ ID NO: 8338	0.01 %	1.215
19	39	SEQ ID NO: 8339	0.00 %	1.2
20	234	SEQ ID NO: 8340	0.00 %	0.9

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	99	SEQ ID NO: 8341	1.33 %	162
2	81	SEQ ID NO: 8342	0.44 %	54
3	104	SEQ ID NO: 8343	0.24 %	30
4	51	SEQ ID NO: 8344	0.16 %	20
5	122	SEQ ID NO: 8345	0.11 %	13.5

6	71	SEQ ID NO: 8346	0.07 %	9
7	69	SEQ ID NO: 8347	0.04 %	6
8	223	SEQ ID NO: 8348	0.04 %	5.4
9	84	SEQ ID NO: 8349	0.03 %	4.5
10	63	SEQ ID NO: 8350	0.02 %	3.6
11	138	SEQ ID NO: 8351	0.02 %	3
12	201	SEQ ID NO: 8352	0.01 %	1.8
13	44	SEQ ID NO: 8353	0.01 %	1.35
14	83	SEQ ID NO: 8354	0.01 %	1.35
15	116	SEQ ID NO: 8355	0.00 %	1.2
16	46	SEQ ID NO: 8356	0.00 %	0.9
17	183	SEQ ID NO: 8357	0.00 %	0.81
18	57	SEQ ID NO: 8358	0.00 %	0.6
19	93	SEQ ID NO: 8359	0.00 %	0.6
20	113	SEQ ID NO: 8360	0.00 %	0.6

HLA A24 - 9 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	198	SEQ ID NO: 8361	13.15 %	210
2	105	SEQ ID NO: 8362	9.39 %	150
3	210	SEQ ID NO: 8363	4.69 %	75
4	75	SEQ ID NO: 8364	3.15 %	50.4
5	85	SEQ ID NO: 8365	2.63 %	42
6	205	SEQ ID NO: 8366	2.10 %	33.6
7	77	SEQ ID NO: 8367	1.87 %	30
8	158	SEQ ID NO: 8368	0.65 %	10.5
9	103	SEQ ID NO: 8369	0.56 %	9
10	227	SEQ ID NO: 8370	0.55 %	8.8704
11	32	SEQ ID NO: 8371	0.54 %	8.64
12	74	SEQ ID NO: 8372	0.50 %	8
13	131	SEQ ID NO: 8373	0.50 %	8
14	54	SEQ ID NO: 8374	0.46 %	7.5
15	99	SEQ ID NO: 8375	0.45 %	7.2
16	44	SEQ ID NO: 8376	0.37 %	6
17	62	SEQ ID NO: 8377	0.37 %	6
18	87	SEQ ID NO: 8378	0.37 %	6
19	89	SEQ ID NO: 8379	0.37 %	6
20	154	SEQ ID NO: 8380	0.37 %	6

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	105	SEQ ID NO: 8381	22.54 %	360
2	204	SEQ ID NO: 8382	17.53 %	280
3	209	SEQ ID NO: 8383	3.13 %	50
4	75	SEQ ID NO: 8384	1.87 %	30
5	85	SEQ ID NO: 8385	1.87 %	30
6	77	SEQ ID NO: 8386	1.12 %	18
7	74	SEQ ID NO: 8387	0.84 %	13.44
8	210	SEQ ID NO: 8388	0.56 %	9
9	226	SEQ ID NO: 8389	0.55 %	8.8704
10	98	SEQ ID NO: 8390	0.54 %	8.64
11	198	SEQ ID NO: 8391	0.46 %	7.5
12	67	SEQ ID NO: 8392	0.45 %	7.2
13	152	SEQ ID NO: 8393	0.43 %	7
14	43	SEQ ID NO: 8394	0.37 %	6
15	63	SEQ ID NO: 8395	0.37 %	6
16	72	SEQ ID NO: 8396	0.37 %	6
17	89	SEQ ID NO: 8397	0.37 %	6
18	101	SEQ ID NO: 8398	0.37 %	6
19	107	SEQ ID NO: 8399	0.37 %	6
20	111	SEQ ID NO: 8400	0.37 %	6

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	138	SEQ ID NO: 8401	0.21 %	8532.082944
2	106	SEQ ID NO: 8402	0.10 %	3977.8497792
3	44	SEQ ID NO: 8403	0.03 %	1243.078056
4	71	SEQ ID NO: 8404	0.00 %	348.872832
5	234	SEQ ID NO: 8405	0.00 %	243.432
6	51	SEQ ID NO: 8406	0.00 %	130.26096
7	109	SEQ ID NO: 8407	0.00 %	91.182672
8	81	SEQ ID NO: 8408	0.00 %	73.342584
9	88	SEQ ID NO: 8409	0.00 %	70.386624
10	1	SEQ ID NO: 8410	0.00 %	65.32728732
11	38	SEQ ID NO: 8411	0.00 %	47.876409

12	76	SEQ ID NO: 8412	0.00 %	36.8637882
13	46	SEQ ID NO: 8413	0.00 %	30.889782
14	211	SEQ ID NO: 8414	0.00 %	21.616753941
15	201	SEQ ID NO: 8415	0.00 %	19.657134
16	102	SEQ ID NO: 8416	0.00 %	18.4318941
17	199	SEQ ID NO: 8417	0.00 %	16.496865
18	74	SEQ ID NO: 8418	0.00 %	15.783256167
19	62	SEQ ID NO: 8419	0.00 %	13.9968225
20	99	SEQ ID NO: 8420	0.00 %	10.31851392

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	78	SEQ ID NO: 8421	0.01 %	556.494246
2	138	SEQ ID NO: 8422	0.01 %	395.245972224
3	84	SEQ ID NO: 8423	0.00 %	201.554244
4	71	SEQ ID NO: 8424	0.00 %	143.65707264
5	44	SEQ ID NO: 8425	0.00 %	132.54624
6	76	SEQ ID NO: 8426	0.00 %	84.78671286
7	8	SEQ ID NO: 8427	0.00 %	69.552
8	211	SEQ ID NO: 8428	0.00 %	52.7237901
9	113	SEQ ID NO: 8429	0.00 %	47.99088
10	61	SEQ ID NO: 8430	0.00 %	37.4509575
11	93	SEQ ID NO: 8431	0.00 %	31.24872
12	137	SEQ ID NO: 8432	0.00 %	31.1384304
13	37	SEQ ID NO: 8433	0.00 %	27.531
14	55	SEQ ID NO: 8434	0.00 %	22.9153278
15	98	SEQ ID NO: 8435	0.00 %	22.1063618985
16	108	SEQ ID NO: 8436	0.00 %	21.55457052
17	63	SEQ ID NO: 8437	0.00 %	21.3624
18	45	SEQ ID NO: 8438	0.00 %	19.657134
19	200	SEQ ID NO: 8439	0.00 %	19.657134
20	104	SEQ ID NO: 8440	0.00 %	13.87622016

HLA A 1101 - 9 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	58	SEQ ID NO: 8441	5.55 %	2
2	125	SEQ ID NO: 8442	1.66 %	0.6

3	226	SEQ ID NO: 8443	1.66 %	0.6
4	229	SEQ ID NO: 8444	1.66 %	0.6

HLA A 1101 - 10 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	122	SEQ ID NO: 8445	2.22 %	0.8
2	228	SEQ ID NO: 8446	2.22 %	0.8

HLA B7 - 9 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	97	SEQ ID NO: 8447	0.66 %	36
2	86	SEQ ID NO: 8448	0.37 %	20
3	37	SEQ ID NO: 8449	0.33 %	18
4	62	SEQ ID NO: 8450	0.33 %	18
5	32	SEQ ID NO: 8451	0.22 %	12
6	102	SEQ ID NO: 8452	0.22 %	12
7	227	SEQ ID NO: 8453	0.22 %	12
8	53	SEQ ID NO: 8454	0.11 %	6
9	1	SEQ ID NO: 8455	0.07 %	4
10	44	SEQ ID NO: 8456	0.07 %	4
11	56	SEQ ID NO: 8457	0.07 %	4
12	64	SEQ ID NO: 8458	0.07 %	4
13	74	SEQ ID NO: 8459	0.07 %	4
14	76	SEQ ID NO: 8460	0.07 %	4
15	87	SEQ ID NO: 8461	0.07 %	4
16	106	SEQ ID NO: 8462	0.07 %	4
17	131	SEQ ID NO: 8463	0.07 %	4
18	23	SEQ ID NO: 8464	0.03 %	2
19	157	SEQ ID NO: 8465	0.03 %	2
20	166	SEQ ID NO: 8466	0.03 %	2

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	119	SEQ ID NO: 8467	3.33 %	180
2	264	SEQ ID NO: 8468	1.48 %	80
3	98	SEQ ID NO: 8469	0.66 %	36

4	27	SEQ ID NO: 8470	0.37 %	20
5	86	SEQ ID NO: 8471	0.37 %	20
6	31	SEQ ID NO: 8472	0.22 %	12
7	63	SEQ ID NO: 8473	0.22 %	12
8	96	SEQ ID NO: 8474	0.22 %	12
9	101	SEQ ID NO: 8475	0.22 %	12
10	226	SEQ ID NO: 8476	0.22 %	12
11	157	SEQ ID NO: 8477	0.14 %	8
12	176	SEQ ID NO: 8478	0.14 %	8
13	238	SEQ ID NO: 8479	0.14 %	8
14	36	SEQ ID NO: 8480	0.11 %	6
15	53	SEQ ID NO: 8481	0.11 %	6
16	61	SEQ ID NO: 8482	0.11 %	6
17	3	SEQ ID NO: 8483	0.07 %	4
18	40	SEQ ID NO: 8484	0.07 %	4
19	55	SEQ ID NO: 8485	0.07 %	4
20	74	SEQ ID NO: 8486	0.07 %	4

Table 18: Epitopes for SEQ ID NO: 6044

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	69	SEQ ID NO: 8487	0.04 %	2.5
2	89	SEQ ID NO: 8488	0.02 %	1.5
3	141	SEQ ID NO: 8489	0.01 %	1
4	113	SEQ ID NO: 8490	0.00 %	0.5

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	21	SEQ ID NO: 8491	0.02 %	1.5
2	88	SEQ ID NO: 8492	0.02 %	1.5
3	8	SEQ ID NO: 8493	0.02 %	1.25
4	31	SEQ ID NO: 8494	0.00 %	0.5
5	112	SEQ ID NO: 8495	0.00 %	0.5

HLA A3 - 9 mers

Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	60	SEQ ID NO: 8496	1.23 %	150
2	77	SEQ ID NO: 8497	1.11 %	135
3	141	SEQ ID NO: 8498	0.49 %	60
4	95	SEQ ID NO: 8499	0.32 %	40
5	128	SEQ ID NO: 8500	0.08 %	10
6	113	SEQ ID NO: 8501	0.04 %	6
7	69	SEQ ID NO: 8502	0.01 %	2
8	22	SEQ ID NO: 8503	0.01 %	1.8
9	42	SEQ ID NO: 8504	0.01 %	1.8
10	78	SEQ ID NO: 8505	0.00 %	1.2
11	32	SEQ ID NO: 8506	0.00 %	1
12	54	SEQ ID NO: 8507	0.00 %	0.9
13	74	SEQ ID NO: 8508	0.00 %	0.9
14	28	SEQ ID NO: 8509	0.00 %	0.6
15	36	SEQ ID NO: 8510	0.00 %	0.6
16	48	SEQ ID NO: 8511	0.00 %	0.6
17	118	SEQ ID NO: 8512	0.00 %	0.6
18	4	SEQ ID NO: 8513	0.00 %	0.5

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	94	SEQ ID NO: 8514	0.49 %	60
2	48	SEQ ID NO: 8515	0.16 %	20
3	128	SEQ ID NO: 8516	0.16 %	20
4	60	SEQ ID NO: 8517	0.12 %	15
5	127	SEQ ID NO: 8518	0.12 %	15
6	25	SEQ ID NO: 8519	0.04 %	6
7	95	SEQ ID NO: 8520	0.04 %	6
8	141	SEQ ID NO: 8521	0.04 %	6
9	41	SEQ ID NO: 8522	0.04 %	5.4
10	77	SEQ ID NO: 8523	0.04 %	5.4
11	116	SEQ ID NO: 8524	0.04 %	5.4
12	91	SEQ ID NO: 8525	0.03 %	4
13	4	SEQ ID NO: 8526	0.01 %	2
14	112	SEQ ID NO: 8527	0.01 %	1.8
15	113	SEQ ID NO: 8528	0.01 %	1.35

16	12	SEQ ID NO: 8529	0.00 %	1.2
17	31	SEQ ID NO: 8530	0.00 %	1
18	32	SEQ ID NO: 8531	0.00 %	1
19	15	SEQ ID NO: 8532	0.00 %	0.9
20	27	SEQ ID NO: 8533	0.00 %	0.9

HLA A24 - 9 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	61	SEQ ID NO: 8534	14.46 %	231
2	16	SEQ ID NO: 8535	3.13 %	50
3	120	SEQ ID NO: 8536	1.87 %	30
4	41	SEQ ID NO: 8537	0.60 %	9.6
5	71	SEQ ID NO: 8538	0.45 %	7.2
6	21	SEQ ID NO: 8539	0.37 %	6
7	53	SEQ ID NO: 8540	0.37 %	6
8	65	SEQ ID NO: 8541	0.37 %	6
9	121	SEQ ID NO: 8542	0.37 %	6
10	74	SEQ ID NO: 8543	0.36 %	5.76
11	20	SEQ ID NO: 8544	0.35 %	5.6
12	79	SEQ ID NO: 8545	0.35 %	5.6
13	105	SEQ ID NO: 8546	0.33 %	5.28
14	48	SEQ ID NO: 8547	0.30 %	4.8
15	88	SEQ ID NO: 8548	0.30 %	4.8
16	106	SEQ ID NO: 8549	0.30 %	4.8
17	37	SEQ ID NO: 8550	0.27 %	4.4
18	70	SEQ ID NO: 8551	0.27 %	4.4
19	18	SEQ ID NO: 8552	0.25 %	4
20	57	SEQ ID NO: 8553	0.22 %	3.6

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	120	SEQ ID NO: 8554	1.87 %	30
2	73	SEQ ID NO: 8555	0.54 %	8.64
3	19	SEQ ID NO: 8556	0.52 %	8.4
4	78	SEQ ID NO: 8557	0.52 %	8.4
5	104	SEQ ID NO: 8558	0.49 %	7.92
6	61	SEQ ID NO: 8559	0.46 %	7.5

7	47	SEQ ID NO: 8560	0.45 %	7.2
8	36	SEQ ID NO: 8561	0.41 %	6.6
9	52	SEQ ID NO: 8562	0.37 %	6
10	64	SEQ ID NO: 8563	0.30 %	4.8
11	70	SEQ ID NO: 8564	0.30 %	4.8
12	105	SEQ ID NO: 8565	0.30 %	4.8
13	123	SEQ ID NO: 8566	0.30 %	4.8
14	69	SEQ ID NO: 8567	0.27 %	4.4
15	20	SEQ ID NO: 8568	0.25 %	4
16	66	SEQ ID NO: 8569	0.25 %	4
17	83	SEQ ID NO: 8570	0.25 %	4
18	86	SEQ ID NO: 8571	0.25 %	4
19	101	SEQ ID NO: 8572	0.25 %	4
20	119	SEQ ID NO: 8573	0.25 %	4

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	62	SEQ ID NO: 8574	0.00 %	136.1646
2	85	SEQ ID NO: 8575	0.00 %	69.6969
3	47	SEQ ID NO: 8576	0.00 %	60.153786
4	121	SEQ ID NO: 8577	0.00 %	52.5182736
5	74	SEQ ID NO: 8578	0.00 %	49.13352
6	23	SEQ ID NO: 8579	0.00 %	21.99582
7	78	SEQ ID NO: 8580	0.00 %	19.42488
8	114	SEQ ID NO: 8581	0.00 %	14.6900655
9	4	SEQ ID NO: 8582	0.00 %	11.304684
10	79	SEQ ID NO: 8583	0.00 %	8.4687081
11	122	SEQ ID NO: 8584	0.00 %	6.0996
12	100	SEQ ID NO: 8585	0.00 %	5.382
13	105	SEQ ID NO: 8586	0.00 %	4.981593
14	25	SEQ ID NO: 8587	0.00 %	4.968
15	115	SEQ ID NO: 8588	0.00 %	4.966482
16	24	SEQ ID NO: 8589	0.00 %	4.4815221585
17	111	SEQ ID NO: 8590	0.00 %	4.128201
18	94	SEQ ID NO: 8591	0.00 %	3.67632
19	34	SEQ ID NO: 8592	0.00 %	3.47553
20	12	SEQ ID NO: 8593	0.00 %	3.30993

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	77	SEQ ID NO: 8594	0.00 %	147.97188
2	62	SEQ ID NO: 8595	0.00 %	143.59176
3	113	SEQ ID NO: 8596	0.00 %	106.83684
4	78	SEQ ID NO: 8597	0.00 %	83.526984
5	86	SEQ ID NO: 8598	0.00 %	83.526984
6	74	SEQ ID NO: 8599	0.00 %	69.552
7	121	SEQ ID NO: 8600	0.00 %	61.06776
8	12	SEQ ID NO: 8601	0.00 %	50.232
9	44	SEQ ID NO: 8602	0.00 %	26.082
10	4	SEQ ID NO: 8603	0.00 %	18.3816
11	0	SEQ ID NO: 8604	0.00 %	17.38386
12	72	SEQ ID NO: 8605	0.00 %	17.1396
13	22	SEQ ID NO: 8606	0.00 %	16.21914
14	122	SEQ ID NO: 8607	0.00 %	14.02908
15	64	SEQ ID NO: 8608	0.00 %	11.161854
16	46	SEQ ID NO: 8609	0.00 %	10.34586
17	54	SEQ ID NO: 8610	0.00 %	8.846145
18	47	SEQ ID NO: 8611	0.00 %	7.575080337
19	131	SEQ ID NO: 8612	0.00 %	7.452
20	114	SEQ ID NO: 8613	0.00 %	6.735366

HLA A 1101 - 9 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	69	SEQ ID NO: 8614	5.55 %	2
2	22	SEQ ID NO: 8615	5 %	1.8
3	77	SEQ ID NO: 8616	5 %	1.8
4	141	SEQ ID NO: 8617	3.33 %	1.2
5	60	SEQ ID NO: 8618	2.22 %	0.8
6	95	SEQ ID NO: 8619	2.22 %	0.8
7	36	SEQ ID NO: 8620	1.66 %	0.6

HLA A 1101 - 10 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	41	SEQ ID NO: 8621	3.33 %	1.2

2	68	SEQ ID NO: 8622	3.33 %	1.2
3	94	SEQ ID NO: 8623	3.33 %	1.2
4	31	SEQ ID NO: 8624	2.77 %	1
5	127	SEQ ID NO: 8625	2.5 %	0.9

HLA B7 - 9 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	48	SEQ ID NO: 8626	0.74 %	40
2	20	SEQ ID NO: 8627	0.37 %	20
3	121	SEQ ID NO: 8628	0.33 %	18
4	18	SEQ ID NO: 8629	0.07 %	4
5	21	SEQ ID NO: 8630	0.07 %	4
6	37	SEQ ID NO: 8631	0.07 %	4
7	41	SEQ ID NO: 8632	0.07 %	4
8	53	SEQ ID NO: 8633	0.07 %	4
9	65	SEQ ID NO: 8634	0.07 %	4
10	70	SEQ ID NO: 8635	0.07 %	4
11	71	SEQ ID NO: 8636	0.07 %	4
12	74	SEQ ID NO: 8637	0.07 %	4
13	79	SEQ ID NO: 8638	0.07 %	4
14	88	SEQ ID NO: 8639	0.07 %	4
15	105	SEQ ID NO: 8640	0.07 %	4
16	106	SEQ ID NO: 8641	0.07 %	4
17	124	SEQ ID NO: 8642	0.07 %	4
18	1	SEQ ID NO: 8643	0.03 %	2
19	120	SEQ ID NO: 8644	0.03 %	1.8
20	11	SEQ ID NO: 8645	0.02 %	1.2

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	66	SEQ ID NO: 8646	1.48 %	80
2	123	SEQ ID NO: 8647	0.74 %	40
3	20	SEQ ID NO: 8648	0.37 %	20
4	64	SEQ ID NO: 8649	0.22 %	12
5	119	SEQ ID NO: 8650	0.11 %	6
6	54	SEQ ID NO: 8651	0.09 %	5
7	19	SEQ ID NO: 8652	0.07 %	4

8	36	SEQ ID NO: 8653	0.07 %	4
9	47	SEQ ID NO: 8654	0.07 %	4
10	52	SEQ ID NO: 8655	0.07 %	4
11	69	SEQ ID NO: 8656	0.07 %	4
12	70	SEQ ID NO: 8657	0.07 %	4
13	73	SEQ ID NO: 8658	0.07 %	4
14	78	SEQ ID NO: 8659	0.07 %	4
15	83	SEQ ID NO: 8660	0.07 %	4
16	86	SEQ ID NO: 8661	0.07 %	4
17	101	SEQ ID NO: 8662	0.07 %	4
18	104	SEQ ID NO: 8663	0.07 %	4
19	105	SEQ ID NO: 8664	0.07 %	4
20	15	SEQ ID NO: 8665	0.03 %	2

Table 19: Epitopes for SEQ ID NO: 6045

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	4	SEQ ID NO: 8666	0.02 %	1.35
2	66	SEQ ID NO: 8667	0.02 %	1.35
3	33	SEQ ID NO: 8668	0.02 %	1.25
4	44	SEQ ID NO: 8669	0.01 %	1
5	50	SEQ ID NO: 8670	0.01 %	1
6	14	SEQ ID NO: 8671	0.01 %	0.75
7	48	SEQ ID NO: 8672	0.01 %	0.75
8	11	SEQ ID NO: 8673	0.00 %	0.5

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	4	SEQ ID NO: 8674	0.12 %	6.75
2	66	SEQ ID NO: 8675	0.12 %	6.75
3	10	SEQ ID NO: 8676	0.00 %	0.5
4	28	SEQ ID NO: 8677	0.00 %	0.5
5	32	SEQ ID NO: 8678	0.00 %	0.5
6	47	SEQ ID NO: 8679	0.00 %	0.5

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	17	SEQ ID NO: 8680	0.24 %	30
2	44	SEQ ID NO: 8681	0.07 %	9
3	19	SEQ ID NO: 8682	0.06 %	8.1
4	50	SEQ ID NO: 8683	0.04 %	5.4
5	29	SEQ ID NO: 8684	0.03 %	4
6	52	SEQ ID NO: 8685	0.02 %	3.24
7	54	SEQ ID NO: 8686	0.02 %	3
8	11	SEQ ID NO: 8687	0.01 %	1.8
9	37	SEQ ID NO: 8688	0.01 %	1.8
10	25	SEQ ID NO: 8689	0.01 %	1.35
11	10	SEQ ID NO: 8690	0.00 %	0.9
12	16	SEQ ID NO: 8691	0.00 %	0.9
13	35	SEQ ID NO: 8692	0.00 %	0.6

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	49	SEQ ID NO: 8693	0.44 %	54
2	17	SEQ ID NO: 8694	0.22 %	27
3	10	SEQ ID NO: 8695	0.14 %	18
4	16	SEQ ID NO: 8696	0.07 %	9
5	32	SEQ ID NO: 8697	0.04 %	6
6	19	SEQ ID NO: 8698	0.01 %	1.8
7	29	SEQ ID NO: 8699	0.00 %	1.2
8	23	SEQ ID NO: 8700	0.00 %	0.9
9	26	SEQ ID NO: 8701	0.00 %	0.9

HLA A24 - 9 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	18	SEQ ID NO: 8702	1.87 %	30
2	24	SEQ ID NO: 8703	0.65 %	10.5
3	9	SEQ ID NO: 8704	0.52 %	8.4
4	12	SEQ ID NO: 8705	0.52 %	8.4
5	28	SEQ ID NO: 8706	0.52 %	8.4
6	42	SEQ ID NO: 8707	0.52 %	8.4

7	57	SEQ ID NO: 8708	0.52 %	8.4
8	66	SEQ ID NO: 8709	0.52 %	8.4
9	55	SEQ ID NO: 8710	0.51 %	8.25
10	0	SEQ ID NO: 8711	0.48 %	7.7
11	22	SEQ ID NO: 8712	0.45 %	7.2
12	10	SEQ ID NO: 8713	0.37 %	6
13	25	SEQ ID NO: 8714	0.37 %	6
14	30	SEQ ID NO: 8715	0.37 %	6
15	19	SEQ ID NO: 8716	0.35 %	5.6
16	40	SEQ ID NO: 8717	0.31 %	5
17	3	SEQ ID NO: 8718	0.30 %	4.8
18	65	SEQ ID NO: 8719	0.30 %	4.8
19	14	SEQ ID NO: 8720	0.27 %	4.32
20	56	SEQ ID NO: 8721	0.25 %	4

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	55	SEQ ID NO: 8722	18.78 %	300
2	18	SEQ ID NO: 8723	2.63 %	42
3	21	SEQ ID NO: 8724	2.25 %	36
4	2	SEQ ID NO: 8725	1.87 %	30
5	24	SEQ ID NO: 8726	1.87 %	30
6	11	SEQ ID NO: 8727	0.52 %	8.4
7	40	SEQ ID NO: 8728	0.52 %	8.4
8	65	SEQ ID NO: 8729	0.42 %	6.72
9	9	SEQ ID NO: 8730	0.37 %	6
10	8	SEQ ID NO: 8731	0.35 %	5.6
11	27	SEQ ID NO: 8732	0.35 %	5.6
12	41	SEQ ID NO: 8733	0.35 %	5.6
13	57	SEQ ID NO: 8734	0.31 %	5
14	17	SEQ ID NO: 8735	0.25 %	4
15	29	SEQ ID NO: 8736	0.25 %	4
16	64	SEQ ID NO: 8737	0.25 %	4
17	16	SEQ ID NO: 8738	0.22 %	3.6
18	10	SEQ ID NO: 8739	0.18 %	3
19	13	SEQ ID NO: 8740	0.18 %	2.88
20	23	SEQ ID NO: 8741	0.08 %	1.4

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	19	SEQ ID NO: 8742	0.03 %	1310.8823136
2	15	SEQ ID NO: 8743	0.02 %	1082.4143022
3	16	SEQ ID NO: 8744	0.02 %	1040.33238624
4	49	SEQ ID NO: 8745	0.00 %	382.536
5	25	SEQ ID NO: 8746	0.00 %	342.863529264
6	56	SEQ ID NO: 8747	0.00 %	63.28397376
7	12	SEQ ID NO: 8748	0.00 %	40.19736105
8	10	SEQ ID NO: 8749	0.00 %	21.3624
9	22	SEQ ID NO: 8750	0.00 %	19.7762418
10	26	SEQ ID NO: 8751	0.00 %	12.6684
11	20	SEQ ID NO: 8752	0.00 %	11.544666
12	37	SEQ ID NO: 8753	0.00 %	10.4328
13	32	SEQ ID NO: 8754	0.00 %	8.4456
14	23	SEQ ID NO: 8755	0.00 %	6.2888049
15	47	SEQ ID NO: 8756	0.00 %	6.0858
16	3	SEQ ID NO: 8757	0.00 %	4.582929078
17	18	SEQ ID NO: 8758	0.00 %	4.4855150505
18	28	SEQ ID NO: 8759	0.00 %	4.2923589
19	62	SEQ ID NO: 8760	0.00 %	2.88098391
20	27	SEQ ID NO: 8761	0.00 %	1.699677

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	17	SEQ ID NO: 8762	0.16 %	6459.14167272
2	19	SEQ ID NO: 8763	0.01 %	607.88448
3	25	SEQ ID NO: 8764	0.00 %	126.83304
4	11	SEQ ID NO: 8765	0.00 %	63.16728165
5	15	SEQ ID NO: 8766	0.00 %	53.54651988
6	37	SEQ ID NO: 8767	0.00 %	28.51632
7	14	SEQ ID NO: 8768	0.00 %	21.8247414
8	29	SEQ ID NO: 8769	0.00 %	21.3624
9	26	SEQ ID NO: 8770	0.00 %	19.42488
10	3	SEQ ID NO: 8771	0.00 %	17.2167282
11	48	SEQ ID NO: 8772	0.00 %	15.7068219
12	12	SEQ ID NO: 8773	0.00 %	9.8581266

13	27	SEQ ID NO: 8774	0.00 %	7.3086111
14	39	SEQ ID NO: 8775	0.00 %	7.10976
15	23	SEQ ID NO: 8776	0.00 %	5.7419523
16	22	SEQ ID NO: 8777	0.00 %	4.599126
17	45	SEQ ID NO: 8778	0.00 %	2.5495155
18	31	SEQ ID NO: 8779	0.00 %	2.52747
19	52	SEQ ID NO: 8780	0.00 %	2.383605
20	20	SEQ ID NO: 8781	0.00 %	2.332847151

HLA A 1101 - 9 mers

Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	44	SEQ ID NO: 8782	3.33 %	1.2

HLA A 1101 - 10 mers

Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score

HLA B7 - 9 mers

Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	3	SEQ ID NO: 8783	0.37 %	20
2	12	SEQ ID NO: 8784	0.37 %	20
3	22	SEQ ID NO: 8785	0.37 %	20
4	56	SEQ ID NO: 8786	0.37 %	20
5	30	SEQ ID NO: 8787	0.22 %	12
6	9	SEQ ID NO: 8788	0.07 %	4
7	10	SEQ ID NO: 8789	0.07 %	4
8	19	SEQ ID NO: 8790	0.07 %	4
9	25	SEQ ID NO: 8791	0.07 %	4
10	28	SEQ ID NO: 8792	0.07 %	4
11	42	SEQ ID NO: 8793	0.07 %	4
12	65	SEQ ID NO: 8794	0.07 %	4
13	35	SEQ ID NO: 8795	0.05 %	3
14	66	SEQ ID NO: 8796	0.02 %	1.2
15	15	SEQ ID NO: 8797	0.01 %	1
16	47	SEQ ID NO: 8798	0.01 %	1
17	20	SEQ ID NO: 8799	0.01 %	0.6
18	23	SEQ ID NO: 8800	0.00 %	0.5

19	27	SEQ ID NO: 8801	0.00 %	0.5
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HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	27	SEQ ID NO: 8802	0.37 %	20
2	8	SEQ ID NO: 8803	0.07 %	4
3	9	SEQ ID NO: 8804	0.07 %	4
4	11	SEQ ID NO: 8805	0.07 %	4
5	17	SEQ ID NO: 8806	0.07 %	4
6	29	SEQ ID NO: 8807	0.07 %	4
7	41	SEQ ID NO: 8808	0.07 %	4
8	52	SEQ ID NO: 8809	0.07 %	4
9	64	SEQ ID NO: 8810	0.07 %	4
10	65	SEQ ID NO: 8811	0.07 %	4
11	3	SEQ ID NO: 8812	0.03 %	2
12	23	SEQ ID NO: 8813	0.03 %	2
13	21	SEQ ID NO: 8814	0.02 %	1.2
14	15	SEQ ID NO: 8815	0.01 %	1
15	35	SEQ ID NO: 8816	0.01 %	0.6
16	39	SEQ ID NO: 8817	0.01 %	0.6
17	12	SEQ ID NO: 8818	0.00 %	0.5
18	22	SEQ ID NO: 8819	0.00 %	0.5
19	45	SEQ ID NO: 8820	0.00 %	0.5

Table 20: Epitopes for SEQ ID NO: 6046

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	186	SEQ ID NO: 8821	2.22 %	125
2	156	SEQ ID NO: 8822	0.88 %	50
3	14	SEQ ID NO: 8823	0.08 %	4.5
4	0	SEQ ID NO: 8824	0.04 %	2.5
5	29	SEQ ID NO: 8825	0.04 %	2.5
6	85	SEQ ID NO: 8826	0.04 %	2.5
7	168	SEQ ID NO: 8827	0.04 %	2.5
8	133	SEQ ID NO: 8828	0.02 %	1.35

9	111	SEQ ID NO: 8829	0.02 %	1.125
10	61	SEQ ID NO: 8830	0.01 %	1
11	7	SEQ ID NO: 8831	0.01 %	0.9
12	131	SEQ ID NO: 8832	0.01 %	0.9
13	211	SEQ ID NO: 8833	0.01 %	0.625
14	4	SEQ ID NO: 8834	0.00 %	0.5
15	43	SEQ ID NO: 8835	0.00 %	0.5
16	95	SEQ ID NO: 8836	0.00 %	0.5
17	136	SEQ ID NO: 8837	0.00 %	0.5

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	133	SEQ ID NO: 8838	0.04 %	2.7
2	84	SEQ ID NO: 8839	0.04 %	2.5
3	167	SEQ ID NO: 8840	0.04 %	2.5
4	186	SEQ ID NO: 8841	0.04 %	2.5
5	131	SEQ ID NO: 8842	0.04 %	2.25
6	14	SEQ ID NO: 8843	0.03 %	1.8
7	205	SEQ ID NO: 8844	0.02 %	1.25
8	111	SEQ ID NO: 8845	0.02 %	1.125
9	60	SEQ ID NO: 8846	0.01 %	1
10	188	SEQ ID NO: 8847	0.01 %	0.75
11	211	SEQ ID NO: 8848	0.01 %	0.625
12	26	SEQ ID NO: 8849	0.00 %	0.5
13	94	SEQ ID NO: 8850	0.00 %	0.5
14	135	SEQ ID NO: 8851	0.00 %	0.5
15	168	SEQ ID NO: 8852	0.00 %	0.5

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	43	SEQ ID NO: 8853	0.24 %	30
2	90	SEQ ID NO: 8854	0.14 %	18
3	148	SEQ ID NO: 8855	0.09 %	12
4	4	SEQ ID NO: 8856	0.05 %	6.75
5	24	SEQ ID NO: 8857	0.04 %	6
6	19	SEQ ID NO: 8858	0.04 %	5.4
7	136	SEQ ID NO: 8859	0.04 %	5.4

8	54	SEQ ID NO: 8860	0.03 %	4.5
9	32	SEQ ID NO: 8861	0.03 %	4
10	14	SEQ ID NO: 8862	0.02 %	3.6
11	59	SEQ ID NO: 8863	0.02 %	3.6
12	88	SEQ ID NO: 8864	0.02 %	3
13	87	SEQ ID NO: 8865	0.02 %	2.7
14	29	SEQ ID NO: 8866	0.01 %	1.8
15	48	SEQ ID NO: 8867	0.01 %	1.8
16	115	SEQ ID NO: 8868	0.01 %	1.8
17	186	SEQ ID NO: 8869	0.01 %	1.8
18	106	SEQ ID NO: 8870	0.01 %	1.5
19	53	SEQ ID NO: 8871	0.01 %	1.35
20	173	SEQ ID NO: 8872	0.00 %	1.2

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	24	SEQ ID NO: 8873	0.22 %	27
2	54	SEQ ID NO: 8874	0.18 %	22.5
3	135	SEQ ID NO: 8875	0.08 %	10.8
4	51	SEQ ID NO: 8876	0.07 %	9
5	13	SEQ ID NO: 8877	0.06 %	8.1
6	26	SEQ ID NO: 8878	0.04 %	6
7	31	SEQ ID NO: 8879	0.04 %	6
8	90	SEQ ID NO: 8880	0.04 %	6
9	43	SEQ ID NO: 8881	0.03 %	4.5
10	19	SEQ ID NO: 8882	0.03 %	4.05
11	169	SEQ ID NO: 8883	0.02 %	3
12	87	SEQ ID NO: 8884	0.02 %	2.7
13	84	SEQ ID NO: 8885	0.01 %	1.8
14	88	SEQ ID NO: 8886	0.01 %	1.8
15	94	SEQ ID NO: 8887	0.01 %	1.8
16	64	SEQ ID NO: 8888	0.00 %	1.2
17	131	SEQ ID NO: 8889	0.00 %	1.2
18	99	SEQ ID NO: 8890	0.00 %	1
19	53	SEQ ID NO: 8891	0.00 %	0.9
20	85	SEQ ID NO: 8892	0.00 %	0.9

HLA A24 - 9 mers

Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	196	SEQ ID NO: 8893	27.55 %	440
2	44	SEQ ID NO: 8894	18.78 %	300
3	36	SEQ ID NO: 8895	12.52 %	200
4	92	SEQ ID NO: 8896	12.52 %	200
5	109	SEQ ID NO: 8897	2.70 %	43.2
6	25	SEQ ID NO: 8898	1.87 %	30
7	93	SEQ ID NO: 8899	1.12 %	18
8	12	SEQ ID NO: 8900	0.75 %	12
9	123	SEQ ID NO: 8901	0.70 %	11.2
10	7	SEQ ID NO: 8902	0.64 %	10.368
11	17	SEQ ID NO: 8903	0.52 %	8.4
12	139	SEQ ID NO: 8904	0.52 %	8.4
13	193	SEQ ID NO: 8905	0.46 %	7.5
14	6	SEQ ID NO: 8906	0.45 %	7.2
15	19	SEQ ID NO: 8907	0.45 %	7.2
16	110	SEQ ID NO: 8908	0.45 %	7.2
17	114	SEQ ID NO: 8909	0.45 %	7.2
18	210	SEQ ID NO: 8910	0.45 %	7.2
19	46	SEQ ID NO: 8911	0.42 %	6.72
20	52	SEQ ID NO: 8912	0.37 %	6

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	92	SEQ ID NO: 8913	7.51 %	120
2	42	SEQ ID NO: 8914	2.63 %	42
3	109	SEQ ID NO: 8915	2.25 %	36
4	23	SEQ ID NO: 8916	1.87 %	30
5	34	SEQ ID NO: 8917	0.75 %	12
6	6	SEQ ID NO: 8918	0.64 %	10.368
7	45	SEQ ID NO: 8919	0.63 %	10.08
8	196	SEQ ID NO: 8920	0.62 %	10
9	44	SEQ ID NO: 8921	0.56 %	9
10	40	SEQ ID NO: 8922	0.55 %	8.8
11	62	SEQ ID NO: 8923	0.46 %	7.5
12	193	SEQ ID NO: 8924	0.46 %	7.5
13	18	SEQ ID NO: 8925	0.45 %	7.2

14	113	SEQ ID NO: 8926	0.45 %	7.2
15	56	SEQ ID NO: 8927	0.37 %	6
16	176	SEQ ID NO: 8928	0.37 %	6
17	16	SEQ ID NO: 8929	0.35 %	5.6
18	138	SEQ ID NO: 8930	0.35 %	5.6
19	127	SEQ ID NO: 8931	0.33 %	5.28
20	36	SEQ ID NO: 8932	0.31 %	5

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	13	SEQ ID NO: 8933	0.04 %	1793.676528
2	87	SEQ ID NO: 8934	0.03 %	1415.3832
3	24	SEQ ID NO: 8935	0.01 %	618.0996816
4	19	SEQ ID NO: 8936	0.00 %	223.23708
5	12	SEQ ID NO: 8937	0.00 %	210.36400875
6	51	SEQ ID NO: 8938	0.00 %	198.30859992
7	53	SEQ ID NO: 8939	0.00 %	194.477328
8	88	SEQ ID NO: 8940	0.00 %	180.58536756
9	106	SEQ ID NO: 8941	0.00 %	169.74828
10	54	SEQ ID NO: 8942	0.00 %	70.09848
11	59	SEQ ID NO: 8943	0.00 %	43.42032
12	94	SEQ ID NO: 8944	0.00 %	41.792058
13	20	SEQ ID NO: 8945	0.00 %	37.46088108
14	63	SEQ ID NO: 8946	0.00 %	35.73520902
15	22	SEQ ID NO: 8947	0.00 %	20.5916435109
16	47	SEQ ID NO: 8948	0.00 %	12.233222865
17	66	SEQ ID NO: 8949	0.00 %	12.2199
18	56	SEQ ID NO: 8950	0.00 %	11.486706
19	67	SEQ ID NO: 8951	0.00 %	6.416172
20	117	SEQ ID NO: 8952	0.00 %	5.827464

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	43	SEQ ID NO: 8953	0.10 %	3977.8497792
2	24	SEQ ID NO: 8954	0.02 %	836.2525104
3	51	SEQ ID NO: 8955	0.02 %	815.616432
4	49	SEQ ID NO: 8956	0.01 %	660.3245145

5	19	SEQ ID NO: 8957	0.00 %	251.837856
6	59	SEQ ID NO: 8958	0.00 %	159.9696
7	12	SEQ ID NO: 8959	0.00 %	155.245377
8	45	SEQ ID NO: 8960	0.00 %	141.1974531
9	21	SEQ ID NO: 8961	0.00 %	117.22672269
10	53	SEQ ID NO: 8962	0.00 %	84.55536
11	87	SEQ ID NO: 8963	0.00 %	65.5671672
12	13	SEQ ID NO: 8964	0.00 %	64.88888616
13	153	SEQ ID NO: 8965	0.00 %	49.13352
14	178	SEQ ID NO: 8966	0.00 %	26.082
15	18	SEQ ID NO: 8967	0.00 %	24.802259691
16	116	SEQ ID NO: 8968	0.00 %	21.5616168
17	65	SEQ ID NO: 8969	0.00 %	20.77383
18	86	SEQ ID NO: 8970	0.00 %	15.7068219
19	27	SEQ ID NO: 8971	0.00 %	12.3159135
20	46	SEQ ID NO: 8972	0.00 %	11.45624789925

HLA A 1101 - 9 mers

Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	4	SEQ ID NO: 8973	12.5 %	4.5
2	136	SEQ ID NO: 8974	3.33 %	1.2
3	156	SEQ ID NO: 8975	3.33 %	1.2
4	140	SEQ ID NO: 8976	1.66 %	0.6

HLA A 1101 - 10 mers

Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	169	SEQ ID NO: 8977	5.55 %	2
2	94	SEQ ID NO: 8978	3.33 %	1.2

HLA B7 - 9 mers

Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	146	SEQ ID NO: 8979	0.74 %	40
2	154	SEQ ID NO: 8980	0.74 %	40
3	80	SEQ ID NO: 8981	0.66 %	36
4	139	SEQ ID NO: 8982	0.33 %	18
5	83	SEQ ID NO: 8983	0.22 %	12

6	209	SEQ ID NO: 8984	0.22 %	12
7	7	SEQ ID NO: 8985	0.11 %	6
8	3	SEQ ID NO: 8986	0.07 %	4
9	6	SEQ ID NO: 8987	0.07 %	4
10	12	SEQ ID NO: 8988	0.07 %	4
11	19	SEQ ID NO: 8989	0.07 %	4
12	24	SEQ ID NO: 8990	0.07 %	4
13	38	SEQ ID NO: 8991	0.07 %	4
14	46	SEQ ID NO: 8992	0.07 %	4
15	56	SEQ ID NO: 8993	0.07 %	4
16	110	SEQ ID NO: 8994	0.07 %	4
17	114	SEQ ID NO: 8995	0.07 %	4
18	123	SEQ ID NO: 8996	0.07 %	4
19	129	SEQ ID NO: 8997	0.07 %	4
20	166	SEQ ID NO: 8998	0.07 %	4

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	56	SEQ ID NO: 8999	1.48 %	80
2	40	SEQ ID NO: 9000	0.74 %	40
3	127	SEQ ID NO: 9001	0.74 %	40
4	170	SEQ ID NO: 9002	0.74 %	40
5	140	SEQ ID NO: 9003	0.27 %	15
6	35	SEQ ID NO: 9004	0.22 %	12
7	79	SEQ ID NO: 9005	0.22 %	12
8	82	SEQ ID NO: 9006	0.22 %	12
9	208	SEQ ID NO: 9007	0.22 %	12
10	209	SEQ ID NO: 9008	0.22 %	12
11	80	SEQ ID NO: 9009	0.16 %	9
12	129	SEQ ID NO: 9010	0.14 %	8
13	138	SEQ ID NO: 9011	0.11 %	6
14	73	SEQ ID NO: 9012	0.09 %	5
15	2	SEQ ID NO: 9013	0.07 %	4
16	5	SEQ ID NO: 9014	0.07 %	4
17	6	SEQ ID NO: 9015	0.07 %	4
18	16	SEQ ID NO: 9016	0.07 %	4
19	18	SEQ ID NO: 9017	0.07 %	4
20	24	SEQ ID NO: 9018	0.07 %	4

Table 21: Epitopes for SEQ ID NO: 6047

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	53	SEQ ID NO: 9019	2 %	112.5
2	10	SEQ ID NO: 9020	0.08 %	4.5
3	33	SEQ ID NO: 9021	0.02 %	1.5
4	3	SEQ ID NO: 9022	0.00 %	0.5
5	27	SEQ ID NO: 9023	0.00 %	0.5
6	29	SEQ ID NO: 9024	0.00 %	0.5

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	10	SEQ ID NO: 9025	0.8 %	45
2	52	SEQ ID NO: 9026	0.2 %	11.25
3	50	SEQ ID NO: 9027	0.04 %	2.5
4	32	SEQ ID NO: 9028	0.02 %	1.5
5	48	SEQ ID NO: 9029	0.02 %	1.35
6	27	SEQ ID NO: 9030	0.00 %	0.5

5

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	38	SEQ ID NO: 9031	1.85 %	225
2	17	SEQ ID NO: 9032	0.02 %	3.6
3	2	SEQ ID NO: 9033	0.02 %	2.7
4	37	SEQ ID NO: 9034	0.01 %	1.8
5	27	SEQ ID NO: 9035	0.01 %	1.35
6	13	SEQ ID NO: 9036	0.00 %	0.675
7	14	SEQ ID NO: 9037	0.00 %	0.6

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	13	SEQ ID NO: 9038	0.04 %	6
2	37	SEQ ID NO: 9039	0.01 %	2.025

3	2	SEQ ID NO: 9040	0.00 %	0.9
4	19	SEQ ID NO: 9041	0.00 %	0.675
5	16	SEQ ID NO: 9042	0.00 %	0.54

HLA A24 - 9 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	20	SEQ ID NO: 9043	1.25 %	20
2	6	SEQ ID NO: 9044	0.52 %	8.4
3	5	SEQ ID NO: 9045	0.51 %	8.25
4	35	SEQ ID NO: 9046	0.36 %	5.76
5	31	SEQ ID NO: 9047	0.35 %	5.6
6	43	SEQ ID NO: 9048	0.27 %	4.4
7	13	SEQ ID NO: 9049	0.26 %	4.2
8	32	SEQ ID NO: 9050	0.21 %	3.36
9	2	SEQ ID NO: 9051	0.11 %	1.8
10	9	SEQ ID NO: 9052	0.10 %	1.68
11	8	SEQ ID NO: 9053	0.09 %	1.5
12	15	SEQ ID NO: 9054	0.09 %	1.5
13	23	SEQ ID NO: 9055	0.09 %	1.5
14	27	SEQ ID NO: 9056	0.08 %	1.4
15	24	SEQ ID NO: 9057	0.07 %	1.2
16	7	SEQ ID NO: 9058	0.06 %	1
17	17	SEQ ID NO: 9059	0.06 %	1
18	10	SEQ ID NO: 9060	0.05 %	0.9
19	39	SEQ ID NO: 9061	0.04 %	0.792
20	47	SEQ ID NO: 9062	0.04 %	0.792

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	5	SEQ ID NO: 9063	2.63 %	42
2	34	SEQ ID NO: 9064	0.54 %	8.64
3	30	SEQ ID NO: 9065	0.52 %	8.4
4	19	SEQ ID NO: 9066	0.50 %	8
5	50	SEQ ID NO: 9067	0.33 %	5.28
6	12	SEQ ID NO: 9068	0.26 %	4.2
7	31	SEQ ID NO: 9069	0.21 %	3.36
8	26	SEQ ID NO: 9070	0.15 %	2.52

9	8	SEQ ID NO: 9071	0.13 %	2.1
10	22	SEQ ID NO: 9072	0.12 %	2
11	23	SEQ ID NO: 9073	0.11 %	1.8
12	6	SEQ ID NO: 9074	0.09 %	1.5
13	14	SEQ ID NO: 9075	0.09 %	1.5
14	16	SEQ ID NO: 9076	0.09 %	1.5
15	7	SEQ ID NO: 9077	0.06 %	1
16	48	SEQ ID NO: 9078	0.04 %	0.75
17	0	SEQ ID NO: 9079	0.04 %	0.72
18	9	SEQ ID NO: 9080	0.04 %	0.72
19	47	SEQ ID NO: 9081	0.04 %	0.66
20	39	SEQ ID NO: 9082	0.03 %	0.6

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	15	SEQ ID NO: 9083	0.00 %	14.1442686
2	27	SEQ ID NO: 9084	0.00 %	9.598176
3	22	SEQ ID NO: 9085	0.00 %	9.5634
4	9	SEQ ID NO: 9086	0.00 %	5.546246013
5	2	SEQ ID NO: 9087	0.00 %	5.526462816
6	24	SEQ ID NO: 9088	0.00 %	4.88163753
7	17	SEQ ID NO: 9089	0.00 %	3.699285408
8	31	SEQ ID NO: 9090	0.00 %	2.29699206
9	6	SEQ ID NO: 9091	0.00 %	2.0016040674
10	7	SEQ ID NO: 9092	0.00 %	0.91287
11	49	SEQ ID NO: 9093	0.00 %	0.71805678
12	16	SEQ ID NO: 9094	0.00 %	0.6694257042
13	12	SEQ ID NO: 9095	0.00 %	0.6539828625

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	16	SEQ ID NO: 9096	0.00 %	34.28765802
2	19	SEQ ID NO: 9097	0.00 %	18.9368775
3	14	SEQ ID NO: 9098	0.00 %	14.1442686
4	27	SEQ ID NO: 9099	0.00 %	11.406528
5	26	SEQ ID NO: 9100	0.00 %	10.9304361558
6	34	SEQ ID NO: 9101	0.00 %	5.580927

7	6	SEQ ID NO: 9102	0.00 %	4.865742
8	9	SEQ ID NO: 9103	0.00 %	2.64106953
9	50	SEQ ID NO: 9104	0.00 %	2.6275752
10	30	SEQ ID NO: 9105	0.00 %	2.29699206
11	7	SEQ ID NO: 9106	0.00 %	0.86083641
12	42	SEQ ID NO: 9107	0.00 %	0.7049592
13	22	SEQ ID NO: 9108	0.00 %	0.6628440357
14	2	SEQ ID NO: 9109	0.00 %	0.6530644656

HLA A 1101 - 9 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	37	SEQ ID NO: 9110	15 %	5.4
2	38	SEQ ID NO: 9111	2.22 %	0.8

HLA A 1101 - 10 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	37	SEQ ID NO: 9112	7.5 %	2.7

HLA B7 - 9 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	35	SEQ ID NO: 9113	3.70 %	200
2	17	SEQ ID NO: 9114	0.11 %	6
3	6	SEQ ID NO: 9115	0.07 %	4
4	20	SEQ ID NO: 9116	0.07 %	4
5	31	SEQ ID NO: 9117	0.07 %	4
6	43	SEQ ID NO: 9118	0.07 %	4
7	7	SEQ ID NO: 9119	0.03 %	2
8	23	SEQ ID NO: 9120	0.02 %	1.2
9	24	SEQ ID NO: 9121	0.02 %	1.2
10	10	SEQ ID NO: 9122	0.01 %	0.9

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	35	SEQ ID NO: 9123	0.09 %	5
2	19	SEQ ID NO: 9124	0.07 %	4

3	30	SEQ ID NO: 9125	0.07 %	4
4	34	SEQ ID NO: 9126	0.07 %	4
5	7	SEQ ID NO: 9127	0.03 %	2
6	16	SEQ ID NO: 9128	0.03 %	1.8
7	23	SEQ ID NO: 9129	0.02 %	1.2
8	50	SEQ ID NO: 9130	0.02 %	1.2
9	9	SEQ ID NO: 9131	0.01 %	1

Table 22: Epitopes for SEQ ID NO: 6048

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	66	SEQ ID NO: 9132	0.44 %	25
2	80	SEQ ID NO: 9133	0.08 %	5
3	93	SEQ ID NO: 9134	0.04 %	2.7
4	11	SEQ ID NO: 9135	0.04 %	2.5
5	89	SEQ ID NO: 9136	0.04 %	2.25
6	48	SEQ ID NO: 9137	0.01 %	1
7	3	SEQ ID NO: 9138	0.00 %	0.5
8	9	SEQ ID NO: 9139	0.00 %	0.5
9	56	SEQ ID NO: 9140	0.00 %	0.5
10	101	SEQ ID NO: 9141	0.00 %	0.5
11	106	SEQ ID NO: 9142	0.00 %	0.5
12	110	SEQ ID NO: 9143	0.00 %	0.5

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	30	SEQ ID NO: 9144	0.4 %	22.5
2	88	SEQ ID NO: 9145	0.12 %	6.75
3	48	SEQ ID NO: 9146	0.04 %	2.5
4	55	SEQ ID NO: 9147	0.02 %	1.25
5	13	SEQ ID NO: 9148	0.01 %	0.9
6	79	SEQ ID NO: 9149	0.01 %	0.75
7	93	SEQ ID NO: 9150	0.01 %	0.675
8	2	SEQ ID NO: 9151	0.00 %	0.5
9	8	SEQ ID NO: 9152	0.00 %	0.5

10	65	SEQ ID NO: 9153	0.00 %	0.5
11	66	SEQ ID NO: 9154	0.00 %	0.5
12	80	SEQ ID NO: 9155	0.00 %	0.5
13	105	SEQ ID NO: 9156	0.00 %	0.5
14	109	SEQ ID NO: 9157	0.00 %	0.5

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	109	SEQ ID NO: 9158	0.74 %	90
2	3	SEQ ID NO: 9159	0.24 %	30
3	111	SEQ ID NO: 9160	0.12 %	15
4	106	SEQ ID NO: 9161	0.07 %	9
5	95	SEQ ID NO: 9162	0.05 %	6.075
6	101	SEQ ID NO: 9163	0.04 %	6
7	110	SEQ ID NO: 9164	0.02 %	3.6
8	84	SEQ ID NO: 9165	0.02 %	3
9	80	SEQ ID NO: 9166	0.02 %	2.7
10	37	SEQ ID NO: 9167	0.01 %	2.25
11	9	SEQ ID NO: 9168	0.01 %	2
12	54	SEQ ID NO: 9169	0.01 %	2
13	99	SEQ ID NO: 9170	0.01 %	1.35
14	1	SEQ ID NO: 9171	0.01 %	1.215
15	11	SEQ ID NO: 9172	0.00 %	0.9
16	15	SEQ ID NO: 9173	0.00 %	0.9
17	69	SEQ ID NO: 9174	0.00 %	0.6
18	5	SEQ ID NO: 9175	0.00 %	0.54
19	103	SEQ ID NO: 9176	0.00 %	0.54

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	75	SEQ ID NO: 9177	0.49 %	60
2	109	SEQ ID NO: 9178	0.29 %	36
3	22	SEQ ID NO: 9179	0.14 %	18
4	15	SEQ ID NO: 9180	0.04 %	6
5	110	SEQ ID NO: 9181	0.01 %	2.25
6	95	SEQ ID NO: 9182	0.01 %	1.8
7	101	SEQ ID NO: 9183	0.01 %	1.35

8	43	SEQ ID NO: 9184	0.00 %	1
9	2	SEQ ID NO: 9185	0.00 %	0.9
10	5	SEQ ID NO: 9186	0.00 %	0.9
11	7	SEQ ID NO: 9187	0.00 %	0.9
12	107	SEQ ID NO: 9188	0.00 %	0.9
13	102	SEQ ID NO: 9189	0.00 %	0.81
14	3	SEQ ID NO: 9190	0.00 %	0.75
15	8	SEQ ID NO: 9191	0.00 %	0.6
16	103	SEQ ID NO: 9192	0.00 %	0.54

HLA A24 - 9 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	88	SEQ ID NO: 9193	1.66 %	26.6112
2	77	SEQ ID NO: 9194	0.77 %	12.32
3	18	SEQ ID NO: 9195	0.56 %	9
4	108	SEQ ID NO: 9196	0.56 %	9
5	92	SEQ ID NO: 9197	0.54 %	8.64
6	96	SEQ ID NO: 9198	0.54 %	8.64
7	73	SEQ ID NO: 9199	0.46 %	7.5
8	40	SEQ ID NO: 9200	0.45 %	7.2
9	104	SEQ ID NO: 9201	0.42 %	6.72
10	8	SEQ ID NO: 9202	0.41 %	6.6
11	21	SEQ ID NO: 9203	0.37 %	6
12	102	SEQ ID NO: 9204	0.37 %	6
13	22	SEQ ID NO: 9205	0.25 %	4
14	68	SEQ ID NO: 9206	0.25 %	4
15	106	SEQ ID NO: 9207	0.22 %	3.6
16	1	SEQ ID NO: 9208	0.18 %	3
17	79	SEQ ID NO: 9209	0.18 %	3
18	93	SEQ ID NO: 9210	0.18 %	3
19	101	SEQ ID NO: 9211	0.18 %	3
20	37	SEQ ID NO: 9212	0.15 %	2.4

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	100	SEQ ID NO: 9213	0.93 %	15
2	18	SEQ ID NO: 9214	0.78 %	12.6

3	98	SEQ ID NO: 9215	0.52 %	8.4
4	73	SEQ ID NO: 9216	0.46 %	7.5
5	91	SEQ ID NO: 9217	0.45 %	7.2
6	103	SEQ ID NO: 9218	0.42 %	6.72
7	7	SEQ ID NO: 9219	0.41 %	6.6
8	21	SEQ ID NO: 9220	0.37 %	6
9	46	SEQ ID NO: 9221	0.37 %	6
10	93	SEQ ID NO: 9222	0.37 %	6
11	96	SEQ ID NO: 9223	0.37 %	6
12	101	SEQ ID NO: 9224	0.37 %	6
13	77	SEQ ID NO: 9225	0.25 %	4
14	92	SEQ ID NO: 9226	0.22 %	3.6
15	105	SEQ ID NO: 9227	0.22 %	3.6
16	2	SEQ ID NO: 9228	0.18 %	3
17	53	SEQ ID NO: 9229	0.18 %	3
18	36	SEQ ID NO: 9230	0.12 %	2
19	55	SEQ ID NO: 9231	0.12 %	2
20	102	SEQ ID NO: 9232	0.11 %	1.8

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	84	SEQ ID NO: 9233	0.01 %	441.342216
2	102	SEQ ID NO: 9234	0.00 %	63.16728165
3	107	SEQ ID NO: 9235	0.00 %	51.882640425
4	1	SEQ ID NO: 9236	0.00 %	43.8816609
5	95	SEQ ID NO: 9237	0.00 %	33.40165248
6	2	SEQ ID NO: 9238	0.00 %	24.66305226
7	92	SEQ ID NO: 9239	0.00 %	22.64458905
8	103	SEQ ID NO: 9240	0.00 %	20.70206586
9	47	SEQ ID NO: 9241	0.00 %	11.175953184
10	94	SEQ ID NO: 9242	0.00 %	8.452983
11	15	SEQ ID NO: 9243	0.00 %	8.1793152
12	8	SEQ ID NO: 9244	0.00 %	4.993461
13	5	SEQ ID NO: 9245	0.00 %	4.57284528
14	99	SEQ ID NO: 9246	0.00 %	3.999468528
15	105	SEQ ID NO: 9247	0.00 %	2.231322
16	20	SEQ ID NO: 9248	0.00 %	1.3524
17	62	SEQ ID NO: 9249	0.00 %	0.8631693

18	6	SEQ ID NO: 9250	0.00 %	0.824619
19	57	SEQ ID NO: 9251	0.00 %	0.72105
20	58	SEQ ID NO: 9252	0.00 %	0.7147572

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	101	SEQ ID NO: 9253	0.03 %	1243.078056
2	3	SEQ ID NO: 9254	0.01 %	592.944462
3	106	SEQ ID NO: 9255	0.00 %	94.2678
4	5	SEQ ID NO: 9256	0.00 %	43.42032
5	107	SEQ ID NO: 9257	0.00 %	33.30332334
6	102	SEQ ID NO: 9258	0.00 %	32.53181778
7	54	SEQ ID NO: 9259	0.00 %	27.324
8	7	SEQ ID NO: 9260	0.00 %	21.3624
9	1	SEQ ID NO: 9261	0.00 %	13.723479
10	95	SEQ ID NO: 9262	0.00 %	13.00344192
11	94	SEQ ID NO: 9263	0.00 %	10.01276388
12	99	SEQ ID NO: 9264	0.00 %	5.6615328
13	39	SEQ ID NO: 9265	0.00 %	3.6304212
14	111	SEQ ID NO: 9266	0.00 %	2.53368
15	103	SEQ ID NO: 9267	0.00 %	2.475394803
16	14	SEQ ID NO: 9268	0.00 %	2.4519012
17	19	SEQ ID NO: 9269	0.00 %	2.07604992
18	29	SEQ ID NO: 9270	0.00 %	1.8179154
19	57	SEQ ID NO: 9271	0.00 %	1.52076
20	47	SEQ ID NO: 9272	0.00 %	1.27712376

HLA A 1101 - 9 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	80	SEQ ID NO: 9273	3.33 %	1.2
2	69	SEQ ID NO: 9274	1.66 %	0.6
3	109	SEQ ID NO: 9275	1.66 %	0.6

HLA A 1101 - 10 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	22	SEQ ID NO: 9276	11.11 %	4

HLA B7 - 9 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	22	SEQ ID NO: 9277	3.70 %	200
2	77	SEQ ID NO: 9278	2.22 %	120
3	104	SEQ ID NO: 9279	0.22 %	12
4	40	SEQ ID NO: 9280	0.11 %	6
5	8	SEQ ID NO: 9281	0.07 %	4
6	21	SEQ ID NO: 9282	0.07 %	4
7	68	SEQ ID NO: 9283	0.07 %	4
8	92	SEQ ID NO: 9284	0.07 %	4
9	102	SEQ ID NO: 9285	0.07 %	4
10	46	SEQ ID NO: 9286	0.03 %	2
11	98	SEQ ID NO: 9287	0.03 %	2
12	103	SEQ ID NO: 9288	0.03 %	2
13	88	SEQ ID NO: 9289	0.02 %	1.2
14	105	SEQ ID NO: 9290	0.01 %	0.9
15	43	SEQ ID NO: 9291	0.01 %	0.6
16	79	SEQ ID NO: 9292	0.01 %	0.6
17	95	SEQ ID NO: 9293	0.01 %	0.6
18	107	SEQ ID NO: 9294	0.00 %	0.5

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	46	SEQ ID NO: 9295	1.48 %	80
2	98	SEQ ID NO: 9296	1.48 %	80
3	91	SEQ ID NO: 9297	0.37 %	20
4	103	SEQ ID NO: 9298	0.37 %	20
5	7	SEQ ID NO: 9299	0.07 %	4
6	21	SEQ ID NO: 9300	0.07 %	4
7	101	SEQ ID NO: 9301	0.07 %	4
8	107	SEQ ID NO: 9302	0.03 %	2
9	67	SEQ ID NO: 9303	0.02 %	1.2
10	93	SEQ ID NO: 9304	0.02 %	1.2
11	69	SEQ ID NO: 9305	0.01 %	1
12	39	SEQ ID NO: 9306	0.01 %	0.6
13	77	SEQ ID NO: 9307	0.01 %	0.6

14	22	SEQ ID NO: 9308	0.00 %	0.5
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Table 23: Epitopes for SEQ ID NO: 6049

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	0	SEQ ID NO: 9309	0.2 %	11.25
2	35	SEQ ID NO: 9310	0.01 %	0.9
3	4	SEQ ID NO: 9311	0.00 %	0.5
4	5	SEQ ID NO: 9312	0.00 %	0.5
5	10	SEQ ID NO: 9313	0.00 %	0.5
6	19	SEQ ID NO: 9314	0.00 %	0.5
7	21	SEQ ID NO: 9315	0.00 %	0.5

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	0	SEQ ID NO: 9316	0.2 %	11.25
2	5	SEQ ID NO: 9317	0.04 %	2.5
3	33	SEQ ID NO: 9318	0.02 %	1.5
4	3	SEQ ID NO: 9319	0.02 %	1.25
5	9	SEQ ID NO: 9320	0.00 %	0.5
6	18	SEQ ID NO: 9321	0.00 %	0.5
7	20	SEQ ID NO: 9322	0.00 %	0.5

5

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	4	SEQ ID NO: 9323	0.14 %	18
2	16	SEQ ID NO: 9324	0.11 %	13.5
3	23	SEQ ID NO: 9325	0.06 %	8.1
4	18	SEQ ID NO: 9326	0.03 %	4.05
5	21	SEQ ID NO: 9327	0.01 %	2.025
6	9	SEQ ID NO: 9328	0.01 %	1.8
7	15	SEQ ID NO: 9329	0.01 %	1.8
8	25	SEQ ID NO: 9330	0.01 %	1.8
9	12	SEQ ID NO: 9331	0.00 %	0.9

10	19	SEQ ID NO: 9332	0.00 %	0.9
11	20	SEQ ID NO: 9333	0.00 %	0.9
12	2	SEQ ID NO: 9334	0.00 %	0.81
13	22	SEQ ID NO: 9335	0.00 %	0.81
14	10	SEQ ID NO: 9336	0.00 %	0.6

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	20	SEQ ID NO: 9337	0.16 %	20.25
2	9	SEQ ID NO: 9338	0.09 %	12
3	16	SEQ ID NO: 9339	0.07 %	9
4	18	SEQ ID NO: 9340	0.07 %	9
5	22	SEQ ID NO: 9341	0.06 %	8.1
6	4	SEQ ID NO: 9342	0.03 %	4.05
7	15	SEQ ID NO: 9343	0.03 %	4.05
8	12	SEQ ID NO: 9344	0.02 %	3.6
9	3	SEQ ID NO: 9345	0.00 %	0.9
10	33	SEQ ID NO: 9346	0.00 %	0.6
11	2	SEQ ID NO: 9347	0.00 %	0.54
12	24	SEQ ID NO: 9348	0.00 %	0.54

HLA A24 - 9 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	8	SEQ ID NO: 9349	18.78 %	300
2	11	SEQ ID NO: 9350	1.87 %	30
3	28	SEQ ID NO: 9351	1.50 %	24
4	7	SEQ ID NO: 9352	0.75 %	12
5	17	SEQ ID NO: 9353	0.56 %	9
6	14	SEQ ID NO: 9354	0.46 %	7.5
7	23	SEQ ID NO: 9355	0.37 %	6
8	13	SEQ ID NO: 9356	0.36 %	5.76
9	2	SEQ ID NO: 9357	0.35 %	5.6
10	16	SEQ ID NO: 9358	0.35 %	5.6
11	9	SEQ ID NO: 9359	0.30 %	4.8
12	21	SEQ ID NO: 9360	0.26 %	4.2
13	5	SEQ ID NO: 9361	0.25 %	4
14	4	SEQ ID NO: 9362	0.22 %	3.6

15	0	SEQ ID NO: 9363	0.18 %	3
16	19	SEQ ID NO: 9364	0.18 %	3
17	10	SEQ ID NO: 9365	0.15 %	2.4
18	18	SEQ ID NO: 9366	0.13 %	2.1
19	25	SEQ ID NO: 9367	0.06 %	1.1
20	15	SEQ ID NO: 9368	0.05 %	0.9

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	8	SEQ ID NO: 9369	22.54 %	360
2	7	SEQ ID NO: 9370	1.25 %	20
3	17	SEQ ID NO: 9371	0.65 %	10.5
4	15	SEQ ID NO: 9372	0.52 %	8.4
5	4	SEQ ID NO: 9373	0.45 %	7.2
6	22	SEQ ID NO: 9374	0.37 %	6
7	12	SEQ ID NO: 9375	0.36 %	5.76
8	27	SEQ ID NO: 9376	0.30 %	4.8
9	14	SEQ ID NO: 9377	0.28 %	4.5
10	20	SEQ ID NO: 9378	0.26 %	4.2
11	10	SEQ ID NO: 9379	0.25 %	4
12	3	SEQ ID NO: 9380	0.18 %	3
13	18	SEQ ID NO: 9381	0.18 %	3
14	9	SEQ ID NO: 9382	0.15 %	2.4
15	24	SEQ ID NO: 9383	0.10 %	1.65
16	16	SEQ ID NO: 9384	0.07 %	1.2
17	13	SEQ ID NO: 9385	0.06 %	1
18	11	SEQ ID NO: 9386	0.05 %	0.9
19	1	SEQ ID NO: 9387	0.05 %	0.84

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	12	SEQ ID NO: 9388	0.10 %	4267.988928
2	23	SEQ ID NO: 9389	0.03 %	1360.69088544
3	9	SEQ ID NO: 9390	0.01 %	569.948832
4	16	SEQ ID NO: 9391	0.00 %	309.0498408
5	15	SEQ ID NO: 9392	0.00 %	79.73570448
6	2	SEQ ID NO: 9393	0.00 %	51.109542

7	18	SEQ ID NO: 9394	0.00 %	45.25539984
8	25	SEQ ID NO: 9395	0.00 %	34.28765802
9	22	SEQ ID NO: 9396	0.00 %	26.532116325
10	5	SEQ ID NO: 9397	0.00 %	25.26691266
11	21	SEQ ID NO: 9398	0.00 %	4.72873208445
12	11	SEQ ID NO: 9399	0.00 %	2.638538265
13	8	SEQ ID NO: 9400	0.00 %	2.4274552038
14	4	SEQ ID NO: 9401	0.00 %	1.7415324
15	20	SEQ ID NO: 9402	0.00 %	1.6025526
16	13	SEQ ID NO: 9403	0.00 %	1.453803297
17	35	SEQ ID NO: 9404	0.00 %	1.36878336
18	3	SEQ ID NO: 9405	0.00 %	0.824619
19	33	SEQ ID NO: 9406	0.00 %	0.513774

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	22	SEQ ID NO: 9407	0.09 %	3636.068421648
2	4	SEQ ID NO: 9408	0.02 %	1107.960876
3	15	SEQ ID NO: 9409	0.02 %	836.2525104
4	16	SEQ ID NO: 9410	0.00 %	150.9313176
5	12	SEQ ID NO: 9411	0.00 %	76.55002416
6	1	SEQ ID NO: 9412	0.00 %	49.0273014
7	10	SEQ ID NO: 9413	0.00 %	42.1638414747
8	20	SEQ ID NO: 9414	0.00 %	9.29480508
9	24	SEQ ID NO: 9415	0.00 %	9.2669346
10	13	SEQ ID NO: 9416	0.00 %	7.96581954
11	21	SEQ ID NO: 9417	0.00 %	5.051306761875
12	5	SEQ ID NO: 9418	0.00 %	2.6941464
13	11	SEQ ID NO: 9419	0.00 %	2.3839914
14	34	SEQ ID NO: 9420	0.00 %	1.465422
15	2	SEQ ID NO: 9421	0.00 %	0.70794
16	9	SEQ ID NO: 9422	0.00 %	0.6513048
17	19	SEQ ID NO: 9423	0.00 %	0.51882640425

HLA A 1101 - 9 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score

HLA A 1101 - 10 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	33	SEQ ID NO: 9424	1.66 %	0.6

HLA B7 - 9 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	13	SEQ ID NO: 9425	0.22 %	12
2	2	SEQ ID NO: 9426	0.07 %	4
3	9	SEQ ID NO: 9427	0.07 %	4
4	16	SEQ ID NO: 9428	0.07 %	4
5	23	SEQ ID NO: 9429	0.07 %	4
6	5	SEQ ID NO: 9430	0.02 %	1.2
7	15	SEQ ID NO: 9431	0.01 %	1

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	4	SEQ ID NO: 9432	0.07 %	4
2	10	SEQ ID NO: 9433	0.07 %	4
3	12	SEQ ID NO: 9434	0.07 %	4
4	15	SEQ ID NO: 9435	0.07 %	4
5	22	SEQ ID NO: 9436	0.07 %	4
6	13	SEQ ID NO: 9437	0.02 %	1.2

5 Table 24: Epitopes for SEQ ID NO: 6050

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	47	SEQ ID NO: 9438	0.01 %	0.75
2	21	SEQ ID NO: 9439	0.00 %	0.5
3	53	SEQ ID NO: 9440	0.00 %	0.5

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score

1	16	SEQ ID NO: 9441	0.04 %	2.5
2	71	SEQ ID NO: 9442	0.04 %	2.5
3	47	SEQ ID NO: 9443	0.02 %	1.5
4	62	SEQ ID NO: 9444	0.01 %	0.9
5	20	SEQ ID NO: 9445	0.00 %	0.5
6	38	SEQ ID NO: 9446	0.00 %	0.5

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	54	SEQ ID NO: 9447	0.02 %	2.7
2	17	SEQ ID NO: 9448	0.01 %	2
3	3	SEQ ID NO: 9449	0.01 %	1.8

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	22	SEQ ID NO: 9450	0.09 %	12
2	16	SEQ ID NO: 9451	0.01 %	2
3	54	SEQ ID NO: 9452	0.00 %	0.9

HLA A24 - 9 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	70	SEQ ID NO: 9453	2.10 %	33.6
2	7	SEQ ID NO: 9454	1.12 %	18
3	60	SEQ ID NO: 9455	0.46 %	7.5
4	54	SEQ ID NO: 9456	0.37 %	6
5	14	SEQ ID NO: 9457	0.31 %	5
6	19	SEQ ID NO: 9458	0.30 %	4.8
7	47	SEQ ID NO: 9459	0.30 %	4.8
8	12	SEQ ID NO: 9460	0.25 %	4
9	15	SEQ ID NO: 9461	0.25 %	4
10	67	SEQ ID NO: 9462	0.25 %	4
11	21	SEQ ID NO: 9463	0.18 %	3
12	37	SEQ ID NO: 9464	0.06 %	1
13	27	SEQ ID NO: 9465	0.03 %	0.5

HLA A24 - 10 mers				
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Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	14	SEQ ID NO: 9466	12.52 %	200
2	7	SEQ ID NO: 9467	0.93 %	15
3	11	SEQ ID NO: 9468	0.75 %	12
4	60	SEQ ID NO: 9469	0.56 %	9
5	18	SEQ ID NO: 9470	0.45 %	7.2
6	46	SEQ ID NO: 9471	0.45 %	7.2
7	53	SEQ ID NO: 9472	0.37 %	6
8	69	SEQ ID NO: 9473	0.35 %	5.6
9	66	SEQ ID NO: 9474	0.25 %	4
10	20	SEQ ID NO: 9475	0.12 %	2
11	47	SEQ ID NO: 9476	0.07 %	1.2
12	36	SEQ ID NO: 9477	0.06 %	1
13	26	SEQ ID NO: 9478	0.04 %	0.75
14	70	SEQ ID NO: 9479	0.04 %	0.72

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	54	SEQ ID NO: 9480	0.02 %	881.199
2	26	SEQ ID NO: 9481	0.00 %	95.013
3	61	SEQ ID NO: 9482	0.00 %	93.69648
4	19	SEQ ID NO: 9483	0.00 %	40.2894864
5	74	SEQ ID NO: 9484	0.00 %	12.6684
6	35	SEQ ID NO: 9485	0.00 %	10.34586
7	69	SEQ ID NO: 9486	0.00 %	3.3704706
8	13	SEQ ID NO: 9487	0.00 %	1.656
9	15	SEQ ID NO: 9488	0.00 %	1.47537042
10	68	SEQ ID NO: 9489	0.00 %	0.966
11	22	SEQ ID NO: 9490	0.00 %	0.942678
12	12	SEQ ID NO: 9491	0.00 %	0.7669695
13	36	SEQ ID NO: 9492	0.00 %	0.52661835

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	61	SEQ ID NO: 9493	0.00 %	93.69648
2	25	SEQ ID NO: 9494	0.00 %	63.33035625

3	34	SEQ ID NO: 9495	0.00 %	50.232
4	53	SEQ ID NO: 9496	0.00 %	45.2838375
5	26	SEQ ID NO: 9497	0.00 %	14.35752
6	27	SEQ ID NO: 9498	0.00 %	2.8557858
7	17	SEQ ID NO: 9499	0.00 %	2.3973222
8	36	SEQ ID NO: 9500	0.00 %	1.798209
9	69	SEQ ID NO: 9501	0.00 %	1.03521597
10	67	SEQ ID NO: 9502	0.00 %	0.966
11	68	SEQ ID NO: 9503	0.00 %	0.910938
12	11	SEQ ID NO: 9504	0.00 %	0.7669695

HLA A 1101 - 9 mers

Maximum possible score using this molecule type

36

Rank	Start position	Sequence	% of max. score	Score
1	17	SEQ ID NO: 9505	2.22 %	0.8

HLA A 1101 - 10 mers

Maximum possible score using this molecule type

36

Rank	Start position	Sequence	% of max. score	Score
1	16	SEQ ID NO: 9506	5.55 %	2

HLA B7 - 9 mers

Maximum possible score using this molecule type

5400

Rank	Start position	Sequence	% of max. score	Score
1	27	SEQ ID NO: 9507	0.37 %	20
2	54	SEQ ID NO: 9508	0.22 %	12
3	70	SEQ ID NO: 9509	0.22 %	12
4	67	SEQ ID NO: 9510	0.11 %	6
5	12	SEQ ID NO: 9511	0.07 %	4
6	15	SEQ ID NO: 9512	0.07 %	4
7	19	SEQ ID NO: 9513	0.07 %	4
8	49	SEQ ID NO: 9514	0.03 %	2
9	69	SEQ ID NO: 9515	0.03 %	1.8
10	47	SEQ ID NO: 9516	0.02 %	1.2
11	5	SEQ ID NO: 9517	0.01 %	1
12	9	SEQ ID NO: 9518	0.01 %	1
13	35	SEQ ID NO: 9519	0.01 %	1
14	37	SEQ ID NO: 9520	0.01 %	0.6
15	68	SEQ ID NO: 9521	0.01 %	0.6

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	69	SEQ ID NO: 9522	0.66 %	36
2	53	SEQ ID NO: 9523	0.22 %	12
3	5	SEQ ID NO: 9524	0.13 %	7.5
4	66	SEQ ID NO: 9525	0.11 %	6
5	11	SEQ ID NO: 9526	0.07 %	4
6	27	SEQ ID NO: 9527	0.07 %	4
7	46	SEQ ID NO: 9528	0.07 %	4
8	18	SEQ ID NO: 9529	0.02 %	1.2
9	9	SEQ ID NO: 9530	0.01 %	1
10	26	SEQ ID NO: 9531	0.01 %	1
11	25	SEQ ID NO: 9532	0.01 %	0.75
12	17	SEQ ID NO: 9533	0.01 %	0.6
13	36	SEQ ID NO: 9534	0.01 %	0.6
14	68	SEQ ID NO: 9535	0.01 %	0.6
15	35	SEQ ID NO: 9536	0.00 %	0.5
16	42	SEQ ID NO: 9537	0.00 %	0.5
17	73	SEQ ID NO: 9538	0.00 %	0.5

Table 25: Epitopes for SEQ ID NO: 6052

HLA A1 - 9 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	365	SEQ ID NO: 9539	0.8 %	45
2	397	SEQ ID NO: 9540	0.44 %	25
3	229	SEQ ID NO: 9541	0.32 %	18
4	103	SEQ ID NO: 9542	0.17 %	10
5	338	SEQ ID NO: 9543	0.17 %	10
6	251	SEQ ID NO: 9544	0.16 %	9
7	79	SEQ ID NO: 9545	0.11 %	6.25
8	119	SEQ ID NO: 9546	0.10 %	6
9	361	SEQ ID NO: 9547	0.08 %	5
10	60	SEQ ID NO: 9548	0.04 %	2.25
11	101	SEQ ID NO: 9549	0.04 %	2.25
12	278	SEQ ID NO: 9550	0.04 %	2.25

13	23	SEQ ID NO: 9551	0.02 %	1.25
14	164	SEQ ID NO: 9552	0.02 %	1.25
15	165	SEQ ID NO: 9553	0.02 %	1.25
16	295	SEQ ID NO: 9554	0.02 %	1.25
17	172	SEQ ID NO: 9555	0.01 %	0.9
18	0	SEQ ID NO: 9556	0.01 %	0.75
19	311	SEQ ID NO: 9557	0.01 %	0.75
20	78	SEQ ID NO: 9558	0.01 %	0.625

HLA A1 - 10 mers				
Maximum possible score using this molecule type				5625
Rank	Start position	Sequence	% of max. score	Score
1	114	SEQ ID NO: 9559	1.11 %	62.5
2	134	SEQ ID NO: 9560	0.8 %	45
3	365	SEQ ID NO: 9561	0.8 %	45
4	77	SEQ ID NO: 9562	0.66 %	37.5
5	103	SEQ ID NO: 9563	0.44 %	25
6	23	SEQ ID NO: 9564	0.22 %	12.5
7	338	SEQ ID NO: 9565	0.17 %	10
8	361	SEQ ID NO: 9566	0.17 %	10
9	324	SEQ ID NO: 9567	0.11 %	6.25
10	375	SEQ ID NO: 9568	0.11 %	6.25
11	79	SEQ ID NO: 9569	0.04 %	2.5
12	295	SEQ ID NO: 9570	0.04 %	2.5
13	346	SEQ ID NO: 9571	0.04 %	2.5
14	378	SEQ ID NO: 9572	0.03 %	2
15	251	SEQ ID NO: 9573	0.03 %	1.8
16	214	SEQ ID NO: 9574	0.02 %	1.125
17	160	SEQ ID NO: 9575	0.01 %	1
18	172	SEQ ID NO: 9576	0.01 %	0.9
19	229	SEQ ID NO: 9577	0.01 %	0.9
20	376	SEQ ID NO: 9578	0.01 %	0.9

HLA A3 - 9 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	229	SEQ ID NO: 9579	0.49 %	60
2	361	SEQ ID NO: 9580	0.27 %	33.75
3	330	SEQ ID NO: 9581	0.16 %	20

4	218	SEQ ID NO: 9582	0.09 %	12
5	338	SEQ ID NO: 9583	0.04 %	6
6	352	SEQ ID NO: 9584	0.04 %	6
7	103	SEQ ID NO: 9585	0.04 %	5.4
8	291	SEQ ID NO: 9586	0.01 %	2
9	241	SEQ ID NO: 9587	0.01 %	1.8
10	290	SEQ ID NO: 9588	0.01 %	1.8
11	316	SEQ ID NO: 9589	0.01 %	1.8
12	222	SEQ ID NO: 9590	0.01 %	1.35
13	266	SEQ ID NO: 9591	0.01 %	1.35
14	53	SEQ ID NO: 9592	0.00 %	1
15	100	SEQ ID NO: 9593	0.00 %	0.9
16	138	SEQ ID NO: 9594	0.00 %	0.9
17	240	SEQ ID NO: 9595	0.00 %	0.9
18	119	SEQ ID NO: 9596	0.00 %	0.675
19	44	SEQ ID NO: 9597	0.00 %	0.6
20	161	SEQ ID NO: 9598	0.00 %	0.6

HLA A3 - 10 mers				
Maximum possible score using this molecule type				12150
Rank	Start position	Sequence	% of max. score	Score
1	338	SEQ ID NO: 9599	0.49 %	60
2	160	SEQ ID NO: 9600	0.32 %	40
3	352	SEQ ID NO: 9601	0.24 %	30
4	361	SEQ ID NO: 9602	0.18 %	22.5
5	103	SEQ ID NO: 9603	0.13 %	16.2
6	290	SEQ ID NO: 9604	0.07 %	9
7	351	SEQ ID NO: 9605	0.07 %	9
8	44	SEQ ID NO: 9606	0.04 %	6
9	228	SEQ ID NO: 9607	0.03 %	4.05
10	394	SEQ ID NO: 9608	0.02 %	3
11	240	SEQ ID NO: 9609	0.02 %	2.7
12	100	SEQ ID NO: 9610	0.01 %	1.8
13	114	SEQ ID NO: 9611	0.01 %	1.8
14	93	SEQ ID NO: 9612	0.01 %	1.5
15	134	SEQ ID NO: 9613	0.01 %	1.5
16	221	SEQ ID NO: 9614	0.01 %	1.35
17	330	SEQ ID NO: 9615	0.00 %	1.2
18	112	SEQ ID NO: 9616	0.00 %	0.9

19	218	SEQ ID NO: 9617	0.00 %	0.9
20	55	SEQ ID NO: 9618	0.00 %	0.6

HLA A24 - 9 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	345	SEQ ID NO: 9619	1.50 %	24
2	306	SEQ ID NO: 9620	0.75 %	12
3	222	SEQ ID NO: 9621	0.54 %	8.64
4	111	SEQ ID NO: 9622	0.51 %	8.25
5	159	SEQ ID NO: 9623	0.45 %	7.2
6	219	SEQ ID NO: 9624	0.45 %	7.2
7	283	SEQ ID NO: 9625	0.45 %	7.2
8	266	SEQ ID NO: 9626	0.42 %	6.72
9	56	SEQ ID NO: 9627	0.41 %	6.6
10	131	SEQ ID NO: 9628	0.37 %	6
11	214	SEQ ID NO: 9629	0.37 %	6
12	297	SEQ ID NO: 9630	0.37 %	6
13	86	SEQ ID NO: 9631	0.31 %	5
14	122	SEQ ID NO: 9632	0.31 %	5
15	48	SEQ ID NO: 9633	0.30 %	4.8
16	105	SEQ ID NO: 9634	0.30 %	4.8
17	213	SEQ ID NO: 9635	0.30 %	4.8
18	323	SEQ ID NO: 9636	0.30 %	4.8
19	338	SEQ ID NO: 9637	0.30 %	4.8
20	399	SEQ ID NO: 9638	0.30 %	4.8

HLA A24 - 10 mers				
Maximum possible score using this molecule type				1596.672
Rank	Start position	Sequence	% of max. score	Score
1	65	SEQ ID NO: 9639	0.93 %	15
2	306	SEQ ID NO: 9640	0.75 %	12
3	95	SEQ ID NO: 9641	0.66 %	10.56
4	36	SEQ ID NO: 9642	0.60 %	9.6
5	385	SEQ ID NO: 9643	0.50 %	8
6	111	SEQ ID NO: 9644	0.46 %	7.5
7	104	SEQ ID NO: 9645	0.45 %	7.2
8	214	SEQ ID NO: 9646	0.45 %	7.2
9	221	SEQ ID NO: 9647	0.45 %	7.2

10	277	SEQ ID NO: 9648	0.45 %	7.2
11	150	SEQ ID NO: 9649	0.37 %	6
12	152	SEQ ID NO: 9650	0.37 %	6
13	158	SEQ ID NO: 9651	0.37 %	6
14	171	SEQ ID NO: 9652	0.37 %	6
15	343	SEQ ID NO: 9653	0.37 %	6
16	110	SEQ ID NO: 9654	0.34 %	5.5
17	85	SEQ ID NO: 9655	0.31 %	5
18	47	SEQ ID NO: 9656	0.30 %	4.8
19	213	SEQ ID NO: 9657	0.30 %	4.8
20	218	SEQ ID NO: 9658	0.30 %	4.8

HLA A 0201 - 9 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score
1	222	SEQ ID NO: 9659	0.03 %	1267.10434728
2	226	SEQ ID NO: 9660	0.00 %	69.552
3	316	SEQ ID NO: 9661	0.00 %	50.232
4	351	SEQ ID NO: 9662	0.00 %	31.24872
5	159	SEQ ID NO: 9663	0.00 %	13.6235739
6	406	SEQ ID NO: 9664	0.00 %	11.4264
7	165	SEQ ID NO: 9665	0.00 %	8.14407
8	238	SEQ ID NO: 9666	0.00 %	7.0518
9	138	SEQ ID NO: 9667	0.00 %	5.112072
10	130	SEQ ID NO: 9668	0.00 %	3.00547233
11	303	SEQ ID NO: 9669	0.00 %	2.59578
12	157	SEQ ID NO: 9670	0.00 %	2.412585
13	219	SEQ ID NO: 9671	0.00 %	2.103255861
14	305	SEQ ID NO: 9672	0.00 %	1.86369
15	158	SEQ ID NO: 9673	0.00 %	1.646892
16	331	SEQ ID NO: 9674	0.00 %	1.614048
17	399	SEQ ID NO: 9675	0.00 %	1.442246832
18	324	SEQ ID NO: 9676	0.00 %	1.319625
19	312	SEQ ID NO: 9677	0.00 %	1.233099
20	262	SEQ ID NO: 9678	0.00 %	0.966

HLA A 0201 - 10 mers				
Maximum possible score using this molecule type				3925227.1
Rank	Start position	Sequence	% of max. score	Score

1	221	SEQ ID NO: 9679	0.00 %	309.0498408
2	112	SEQ ID NO: 9680	0.00 %	98.26704
3	330	SEQ ID NO: 9681	0.00 %	98.26704
4	158	SEQ ID NO: 9682	0.00 %	36.31608
5	218	SEQ ID NO: 9683	0.00 %	24.0754248
6	124	SEQ ID NO: 9684	0.00 %	12.2199
7	55	SEQ ID NO: 9685	0.00 %	10.467576
8	315	SEQ ID NO: 9686	0.00 %	7.7274204
9	350	SEQ ID NO: 9687	0.00 %	4.296699
10	405	SEQ ID NO: 9688	0.00 %	4.286487
11	388	SEQ ID NO: 9689	0.00 %	4.054785
12	322	SEQ ID NO: 9690	0.00 %	3.883803
13	130	SEQ ID NO: 9691	0.00 %	3.428691903
14	45	SEQ ID NO: 9692	0.00 %	3.411230625
15	132	SEQ ID NO: 9693	0.00 %	2.99943
16	410	SEQ ID NO: 9694	0.00 %	2.63718
17	316	SEQ ID NO: 9695	0.00 %	2.48686074
18	104	SEQ ID NO: 9696	0.00 %	2.477311485
19	164	SEQ ID NO: 9697	0.00 %	2.2011
20	282	SEQ ID NO: 9698	0.00 %	2.16591

HLA A 1101 - 9 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	361	SEQ ID NO: 9699	16.66 %	6
2	53	SEQ ID NO: 9700	2.77 %	1
3	240	SEQ ID NO: 9701	1.66 %	0.6
4	241	SEQ ID NO: 9702	1.66 %	0.6

HLA A 1101 - 10 mers				
Maximum possible score using this molecule type				36
Rank	Start position	Sequence	% of max. score	Score
1	361	SEQ ID NO: 9703	16.66 %	6
2	93	SEQ ID NO: 9704	8.33 %	3
3	338	SEQ ID NO: 9705	3.33 %	1.2
4	134	SEQ ID NO: 9706	2.77 %	1
5	228	SEQ ID NO: 9707	2.5 %	0.9
6	160	SEQ ID NO: 9708	2.22 %	0.8
7	239	SEQ ID NO: 9709	1.66 %	0.6

8	240	SEQ ID NO: 9710	1.66 %	0.6
9	257	SEQ ID NO: 9711	1.66 %	0.6
10	379	SEQ ID NO: 9712	1.66 %	0.6

HLA B7 - 9 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	105	SEQ ID NO: 9713	14.81 %	800
2	66	SEQ ID NO: 9714	1.48 %	80
3	93	SEQ ID NO: 9715	0.92 %	50
4	257	SEQ ID NO: 9716	0.55 %	30
5	323	SEQ ID NO: 9717	0.37 %	20
6	211	SEQ ID NO: 9718	0.22 %	12
7	219	SEQ ID NO: 9719	0.22 %	12
8	403	SEQ ID NO: 9720	0.18 %	10
9	343	SEQ ID NO: 9721	0.14 %	8
10	12	SEQ ID NO: 9722	0.11 %	6
11	113	SEQ ID NO: 9723	0.11 %	6
12	48	SEQ ID NO: 9724	0.07 %	4
13	56	SEQ ID NO: 9725	0.07 %	4
14	150	SEQ ID NO: 9726	0.07 %	4
15	153	SEQ ID NO: 9727	0.07 %	4
16	159	SEQ ID NO: 9728	0.07 %	4
17	213	SEQ ID NO: 9729	0.07 %	4
18	216	SEQ ID NO: 9730	0.07 %	4
19	222	SEQ ID NO: 9731	0.07 %	4
20	283	SEQ ID NO: 9732	0.07 %	4

HLA B7 - 10 mers				
Maximum possible score using this molecule type				5400
Rank	Start position	Sequence	% of max. score	Score
1	36	SEQ ID NO: 9733	1.48 %	80
2	150	SEQ ID NO: 9734	1.48 %	80
3	343	SEQ ID NO: 9735	1.48 %	80
4	12	SEQ ID NO: 9736	1.11 %	60
5	308	SEQ ID NO: 9737	1.11 %	60
6	130	SEQ ID NO: 9738	0.37 %	20
7	55	SEQ ID NO: 9739	0.22 %	12
8	210	SEQ ID NO: 9740	0.22 %	12

9	218	SEQ ID NO: 9741	0.22 %	12
10	201	SEQ ID NO: 9742	0.18 %	10
11	121	SEQ ID NO: 9743	0.14 %	8
12	391	SEQ ID NO: 9744	0.13 %	7.5
13	112	SEQ ID NO: 9745	0.11 %	6
14	385	SEQ ID NO: 9746	0.11 %	6
15	47	SEQ ID NO: 9747	0.07 %	4
16	66	SEQ ID NO: 9748	0.07 %	4
17	95	SEQ ID NO: 9749	0.07 %	4
18	104	SEQ ID NO: 9750	0.07 %	4
19	152	SEQ ID NO: 9751	0.07 %	4
20	158	SEQ ID NO: 9752	0.07 %	4

TABLE 26: Cloned sequences for *E.coli* expression

ORF	DNA length bp	Cloning	
		pET	pGEX
P28	537	NdeI / XhoI	
P65	1917	NheI / HindIII	
Nsp1A	2495	NheI / XhoI	
Nsp1B	2153	NdeI / XhoI	
Nsp1C	2612	NdeI / XhoI	
Nsp2A	431	NdeI / XhoI	BamHI / XhoI
Nsp2B	426	NdeI / XhoI	BamHI / XhoI
Nsp3	870	NdeI / XhoI	
Nsp4	249	NdeI / XhoI	BamHI / XhoI
Nsp5	594	NheI / XhoI	
Nsp6	339	NdeI / XhoI	BamHI / XhoI
Nsp7	417	NdeI / XhoI	BamHI / XhoI
Nsp9A	1385	NheI / XhoI	
Nsp9B	1409	NdeI / XhoI	
Nsp10	1803	NheI / XhoI	
Nsp11	1581	NdeI / XhoI	
Nsp12	1038	NdeI / HindIII	
Nsp13	897	NdeI / XhoI	
Spike (S1)	1946	NdeI / XhoI	
Spike (S2)	1598	NdeI / XhoI	
Spike (S1-S2)	3545	NdeI / XhoI	
HR1	287	NdeI / XhoI	BamHI / XhoI
HR2	146	NdeI / XhoI	BamHI / XhoI
ORF3Δ100	525	NdeI / XhoI	
ORF4	465	NdeI / XhoI	
Envelope (E)	231	NdeI / XhoI	BamHI / XhoI
Matrix (M)Δ100	366	NdeI / XhoI	BamHI / XhoI
ORF7Δ18	137	NdeI / XhoI	BamHI / XhoI
ORF8	369	NdeI / XhoI	BamHI / XhoI
ORF9	135	NdeI / XhoI	BamHI / XhoI
ORF10	120	NheI / XhoI	BamHI / XhoI
ORF11	255	NdeI / XhoI	BamHI / XhoI
Nucleocapsid (N)	1269	NdeI / EcoRI	
ORF12	297	NdeI / EcoRI	BamHI / EcoRI

TABLE 27: Primers

ORF	Forward primer	Reverse primer
P28	9803	9818
P65	9804	9819
Nsp1A	9805	9820
Nsp1B	9806	9821
Nsp1C	9807	9822
Nsp2 + Nsp3	9808	9823
Nsp4 to Nsp7	9809	9824
Nsp9A	9810	9825
Nsp9B	9811	9826
Nsp10	9812	9827
Nsp11	9813	9828
Nsp12-Nsp13	9814	9829
ORF3-ORF4	9815	9830
Env-ORF10	9816	9831
ORF11-ORF12	9817	9832

TABLE 28: Primers

ORF	Forward primer	Reverse primer
Nsp2A	SEQ ID NO: 9833	SEQ ID NO: 9858
Nsp2B	SEQ ID NO: 9834	SEQ ID NO: 9859
Nsp3	SEQ ID NO: 9835	SEQ ID NO: 9860
Nsp4	SEQ ID NO: 9836	SEQ ID NO: 9861
Nsp5	SEQ ID NO: 9837	SEQ ID NO: 9862
Nsp6	SEQ ID NO: 9838	SEQ ID NO: 9863
Nsp7	SEQ ID NO: 9839	SEQ ID NO: 9864
Nsp12	SEQ ID NO: 9840	SEQ ID NO: 9865
Nsp13	SEQ ID NO: 9841	SEQ ID NO: 9866
Spike S1	SEQ ID NO: 9842	SEQ ID NO: 9867
Spike S2	SEQ ID NO: 9843	SEQ ID NO: 9868
Spike S1-S2	SEQ ID NO: 9844	SEQ ID NO: 9869
HR1	SEQ ID NO: 9845	SEQ ID NO: 9870
HR2	SEQ ID NO: 9846	SEQ ID NO: 9871
Orf3Δ100	SEQ ID NO: 9847	SEQ ID NO: 9872
Orf4	SEQ ID NO: 9848	SEQ ID NO: 9873
Env E	SEQ ID NO: 9849	SEQ ID NO: 9874
Matrix MΔ100	SEQ ID NO: 9850	SEQ ID NO: 9875
Orf7Δ18	SEQ ID NO: 9851	SEQ ID NO: 9876
Orf8	SEQ ID NO: 9852	SEQ ID NO: 9877
Orf9	SEQ ID NO: 9853	SEQ ID NO: 9878
Orf10	SEQ ID NO: 9854	SEQ ID NO: 9879
Orf11	SEQ ID NO: 9855	SEQ ID NO: 9880
Nucleocapsid N	SEQ ID NO: 9856	SEQ ID NO: 9881
Orf12	SEQ ID NO: 9857	SEQ ID NO: 9882

TABLE 29: Cloning, purification and expression in *E.coli*

SARS CoV ORFs	M.W Kd	cloning	Expr.	purification as
P28	19,7	+	+	his sol
P65	70,3	+	+	his sol
Nsp1A (N-term)	91,6	+	+	his ins
Nsp1B (core)	80,8	+	-	
Nsp1C (C-term)	95,3	+	-	
Nsp2A (N-term)	15,8	+	+	his ins
Nsp2B (C-term)	15,5	+	+	his sol
Nsp3	31,9	+	-	
Nsp4	9,1	+	+	his sol
Nsp5	21,8	+	+	his sol
Nsp6	12,4	+	+	his sol
Nsp7	15,3	+	+	his ins
Nsp9A (N-term)	50,8	+	-	
Nsp9B (C-term)	51,6	+	+	his ins
Nsp10	66	-		
Nsp11	58	-		
Nsp12	38	-		
Nsp13	32,7	+	+	his ins
Spike (S1-his)	71,3	+	+	his ins
Spike (S2-his)	58,6	+	-	
Spike (S1S2-his)	130	+	+	his ins
HR1	11	+	+	his ins
HR2	5,4	+	+	his sol
ORF3 $\Delta 100^1$	19,1	+	-	
ORF4	16,9	+	+	his ins (trimer)
Envelope (E)	34,3	+	+	gst ins (IB)
Matrix (M) $\Delta 100$	13,3	+	+	his ins
ORF7 $\Delta 18^2$	31	+	+	gst sol
ORF8	39,5	+	+	gst ins (IB)
ORF9	30,8	+	+	gst sol
ORF10	30,3	+	+	gst ins (IB)
ORF11	35,2	+	+	gst ins (IB)
Nucleocapsid (N)	43,6	+	+	his ins
ORF12	36,7	+	+	his ins

TABLE 30: *E.coli* expression, purity and yield

Protein	Tag	Purity (%)	Yield (mg/l)
Nsp2A (N-term)	His	95	1.7
Nsp2B (C-term)	His	95	4.1
Nsp4	His	95	12.6
Nsp5	His	95	5.88
Nsp6	His	95	8.1
P28	His	95	1
P65	His	80	0.553
HR2	His	95	11.9
HR1	His	80	2.64
Nsp1A	His	95	0.267
Spike S1-S2	His	80	0.381
Matrix M	His	85	12.4
ORF7	GST	85	4.9

TABLE 31: Primers

SEQ ID NO:	Rank	Model	Local	(Position)
10235	F1	1	1	(106)
10236	F2	2	1	(728)
10237	F3	3	1	(112)
10238	F4	5	2	(1331)
10239	F5	6	1	(12)
10240	F6	6	1	(346)
10241	F7	8	1	(904)
10242	F8	9	1	(1016)
10243	F9	9	1	(1015)
10244	F10	9	1	(719)
10245	F11	9	1	(720)
10246	F12	10	1	(724)
10247	R1	2	1	(1283)
10248	R2	4	1	(756)
10249	R3	4	1	(758)
10250	R4	5	2	(259)
10251	R5	6	1	(54)
10252	R6	7	1	(648)
10253	R7	8	1	(948)
10254	R8	8	1	(260)
10255	R9	9	1	(1282)
10256	R10	9	1	(950)
10257	R11	9	1	(756)
10258	R12	10	1	(132)

TABLE 32: Primers

Primers List: (forward)				
Scores				
Rank	Model	Local	Sequence	(Position)
F1	7	1	SEQ ID NO: 10352	(290)
F2	7	1	SEQ ID NO: 10353	(291)
F3	7	1	SEQ ID NO: 10354	(294)
F4	7	1	SEQ ID NO: 10355	(292)
F5	7	1	SEQ ID NO: 10356	(293)
F6	9	1	SEQ ID NO: 10357	(198)
F7	9	1	SEQ ID NO: 10358	(199)
F8	10	1	SEQ ID NO: 10359	(33)
F9	11	1	SEQ ID NO: 10360	(200)
F10	11	1	SEQ ID NO: 10361	(299)
F11	12	1	SEQ ID NO: 10362	(298)
F12	12	1	SEQ ID NO: 10363	(297)
F13	14	1	SEQ ID NO: 10364	(35)
F14	14	1	SEQ ID NO: 10365	(34)
F15	16	1	SEQ ID NO: 10366	(300)
F16	17	1	SEQ ID NO: 10367	(295)
F17	17	1	SEQ ID NO: 10368	(296)
F18	17	1	SEQ ID NO: 10369	(175)
F19	17	1	SEQ ID NO: 10370	(36)
F20	20	1	SEQ ID NO: 10371	(202)
F21	20	1	SEQ ID NO: 10372	(201)
F22	28	1	SEQ ID NO: 10373	(204)
F23	28	1	SEQ ID NO: 10374	(203)
F24	29	1	SEQ ID NO: 10375	(269)
F25	29	1	SEQ ID NO: 10376	(268)
Primers List (reverse)				
Rank	Model	Local	Sequence	(Position)
R1	7	1	SEQ ID NO: 10377	(337)
R2	9	1	SEQ ID NO: 10378	(229)
R3	11	1	SEQ ID NO: 10379	(230)
R4	11	1	SEQ ID NO: 10380	(338)
R5	12	1	SEQ ID NO: 10381	(207)
R6	12	1	SEQ ID NO: 10382	(338)
R7	13	1	SEQ ID NO: 10383	(231)
R8	14	1	SEQ ID NO: 10384	(80)
R9	14	1	SEQ ID NO: 10385	(232)
R10	15	1	SEQ ID NO: 10386	(82)
R11	16	1	SEQ ID NO: 10387	(340)
R12	17	1	SEQ ID NO: 10388	(83)
R13	17	1	SEQ ID NO: 10389	(206)
R14	17	1	SEQ ID NO: 10390	(82)
R15	17	1	SEQ ID NO: 10391	(337)
R16	18	1	SEQ ID NO: 10392	(341)
R17	20	1	SEQ ID NO: 10393	(340)
R18	20	1	SEQ ID NO: 10394	(233)
R19	21	1	SEQ ID NO: 10395	(79)
R20	22	1	SEQ ID NO: 10396	(213)
R21	28	1	SEQ ID NO: 10397	(236)
R22	29	1	SEQ ID NO: 10398	(317)
R23	32	1	SEQ ID NO: 10399	(391)
R24	35	1	SEQ ID NO: 10400	(57)
R25	36	1	SEQ ID NO: 10401	(237)
Primers List (left part): SEQ ID NO ^S : 10402-10433			Primers List (right part): SEQ ID NO ^S : 10434-10464	
Primers List (forward): SEQ ID NO ^S : 10465-10484			Primers List (reverse): SEQ ID NO ^S : 10485-10504	

TABLE 33: Primers

Primers List (forward)				
	Scores			
Rank	Model	Local	Sequence	(Position)
F1	1	1	SEQ ID NO: 10580	(637)
F2	2	1	SEQ ID NO: 10581	(439)
F3	2	1	SEQ ID NO: 10582	(440)
F4	3	1	SEQ ID NO: 10583	(729)
F5	4	1	SEQ ID NO: 10584	(696)
F6	4	1	SEQ ID NO: 10585	(697)
F7	4	1	SEQ ID NO: 10586	(111)
F8	5	1	SEQ ID NO: 10587	(867)
F9	5	1	SEQ ID NO: 10588	(868)
F10	5	1	SEQ ID NO: 10589	(869)
F11	5	1	SEQ ID NO: 10590	(640)
F12	6	1	SEQ ID NO: 10591	(438)
F13	6	1	SEQ ID NO: 10592	(437)
F14	6	1	SEQ ID NO: 10593	(436)
F15	6	1	SEQ ID NO: 10594	(732)
F16	6	1	SEQ ID NO: 10595	(635)
F17	6	1	SEQ ID NO: 10596	(457)
F18	6	1	SEQ ID NO: 10597	(458)
F19	6	1	SEQ ID NO: 10598	(636)
F20	7	1	SEQ ID NO: 10599	(854)
F21	7	1	SEQ ID NO: 10600	(855)
F22	7	1	SEQ ID NO: 10601	(581)
F23	7	1	SEQ ID NO: 10602	(853)
F24	7	1	SEQ ID NO: 10603	(342)
F25	7	1	SEQ ID NO: 10604	(343)
F26	7	1	SEQ ID NO: 10605	(112)
F27	7	1	SEQ ID NO: 10606	(94)
F28	7	1	SEQ ID NO: 10607	(642)
F29	8	1	SEQ ID NO: 10608	(638)
F30	8	1	SEQ ID NO: 10609	(639)
F31	8	1	SEQ ID NO: 10610	(730)
F32	8	1	SEQ ID NO: 10611	(641)
F33	8	1	SEQ ID NO: 10612	(731)
F34	8	1	SEQ ID NO: 10613	(326)
F35	8	1	SEQ ID NO: 10614	(325)
F36	9	1	SEQ ID NO: 10615	(517)
F37	9	1	SEQ ID NO: 10616	(701)
F38	9	1	SEQ ID NO: 10617	(208)
F39	9	1	SEQ ID NO: 10618	(209)
F40	9	1	SEQ ID NO: 10619	(702)
F41	9	1	SEQ ID NO: 10620	(210)
F42	10	1	SEQ ID NO: 10621	(634)
F43	10	1	SEQ ID NO: 10622	(694)
F44	10	1	SEQ ID NO: 10623	(693)
F45	10	1	SEQ ID NO: 10624	(728)
F46	10	1	SEQ ID NO: 10625	(695)
F47	10	1	SEQ ID NO: 10626	(95)
F48	11	1	SEQ ID NO: 10627	(455)
F49	11	1	SEQ ID NO: 10628	(456)
F50	11	1	SEQ ID NO: 10629	(454)

Primers List (reverse)

Rank	Scores		Sequence	(Position)
	Model	Local		
R1	1	1	SEQ ID NO: 10630	(367)
R2	1	1	SEQ ID NO: 10631	(666)
R3	2	1	SEQ ID NO: 10632	(464)
R4	3	1	SEQ ID NO: 10633	(669)
R5	3	1	SEQ ID NO: 10634	(750)
R6	4	1	SEQ ID NO: 10635	(720)
R7	4	1	SEQ ID NO: 10636	(465)
R8	4	1	SEQ ID NO: 10637	(370)
R9	4	1	SEQ ID NO: 10638	(668)
R10	4	1	SEQ ID NO: 10639	(135)
R11	5	1	SEQ ID NO: 10640	(901)
R12	5	1	SEQ ID NO: 10641	(667)
R13	6	1	SEQ ID NO: 10642	(609)
R14	6	1	SEQ ID NO: 10643	(464)
R15	6	1	SEQ ID NO: 10644	(665)
R16	6	1	SEQ ID NO: 10645	(486)
R17	6	1	SEQ ID NO: 10646	(356)
R18	6	1	SEQ ID NO: 10647	(758)
R19	7	1	SEQ ID NO: 10648	(366)
R20	7	1	SEQ ID NO: 10649	(368)
R21	7	1	SEQ ID NO: 10650	(136)
R22	7	1	SEQ ID NO: 10651	(675)
R23	7	1	SEQ ID NO: 10652	(366)
R24	7	1	SEQ ID NO: 10653	(608)
R25	7	1	SEQ ID NO: 10654	(884)
R26	7	1	SEQ ID NO: 10655	(120)
R27	8	1	SEQ ID NO: 10656	(355)
R28	8	1	SEQ ID NO: 10657	(671)
R29	8	1	SEQ ID NO: 10658	(756)
R30	8	1	SEQ ID NO: 10659	(751)
R31	8	1	SEQ ID NO: 10660	(666)
R32	9	1	SEQ ID NO: 10661	(242)
R33	9	1	SEQ ID NO: 10662	(543)
R34	9	1	SEQ ID NO: 10663	(724)
R35	9	1	SEQ ID NO: 10664	(482)
R36	10	1	SEQ ID NO: 10665	(121)
R37	10	1	SEQ ID NO: 10666	(662)
R38	10	1	SEQ ID NO: 10667	(750)
R39	10	1	SEQ ID NO: 10668	(719)
R40	10	1	SEQ ID NO: 10669	(242)
R41	11	1	SEQ ID NO: 10670	(484)
R42	11	1	SEQ ID NO: 10671	(375)
R43	11	1	SEQ ID NO: 10672	(728)
R44	11	1	SEQ ID NO: 10673	(373)
R45	11	1	SEQ ID NO: 10674	(998)
R46	11	1	SEQ ID NO: 10675	(486)
R47	12	1	SEQ ID NO: 10676	(881)
R48	12	1	SEQ ID NO: 10677	(882)
R49	12	1	SEQ ID NO: 10678	(244)
R50	12	1	SEQ ID NO: 10679	(1003)

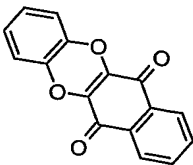
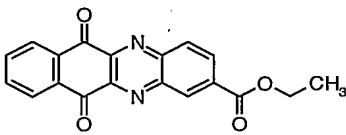
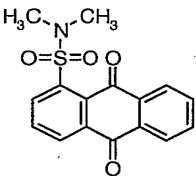
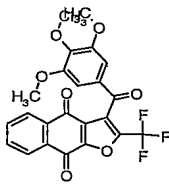
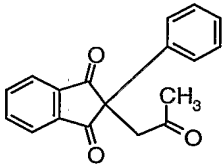
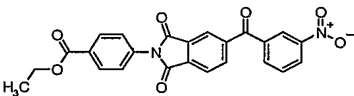
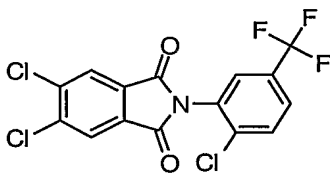
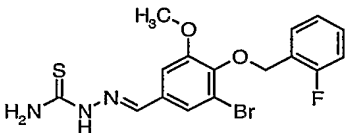
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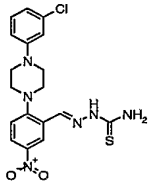
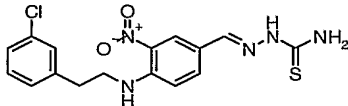
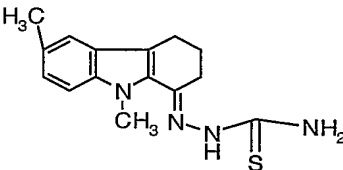
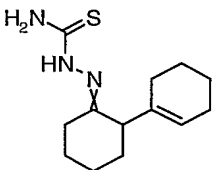
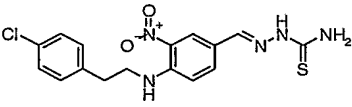
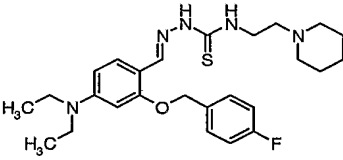
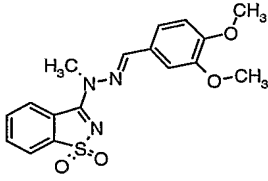
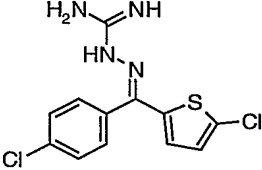
TABLE 34

Compound #	Structure	Name	MH+
1		N-methyl-4-[(2-[(2-(1-methylethyl)phenyl]amino)-1H-benzimidazol-5-yl]oxy]pyridine-2-carboxamide	402.5
2		N-methyl-4-[[1-methyl-2-[(3-(trimethylsilyl)ethynyl]phenyl]amino)-1H-benzimidazol-5-yl]oxy]pyridine-2-carboxamide	470.6
3		N-methyl-4-[(1-methyl-2-[(2-(phenylcarbonyl)phenyl]amino)-1H-benzimidazol-5-yl]oxy]pyridine-2-carboxamide	478.5
4		4-(methyloxy)-N-[6-(methyloxy)-1,3-benzothiazol-2-yl]-3-nitrobenzamide	360.4
5		4-[(2-[(4-butylphenyl)amino]-1,3-benzothiazol-5-yl]oxy)-N-methylpyridine-2-carboxamide	433.5
6		N-methyl-4-[(1-methyl-2-[(6-pyrrolidin-1-ylpyridin-3-yl)amino]-1H-benzimidazol-5-yl]oxy]pyridine-2-carboxamide	444.5
7		4-[(2-[1,1'-bi(cyclohexyl)-2-yl]amino)-1-methyl-1H-benzimidazol-5-yl]oxy)-N-methylpyridine-2-carboxamide	462.6
8		4-[(2-[(4-chlorophenyl)amino]-1-methyl-1H-benzimidazol-5-yl]oxy)-N-1,3-thiazol-2-yl]pyridine-2-carboxamide	477.9

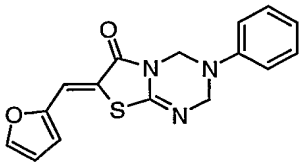
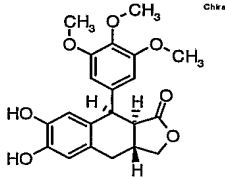
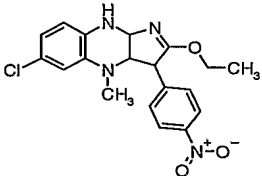
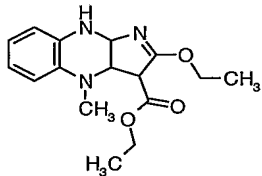
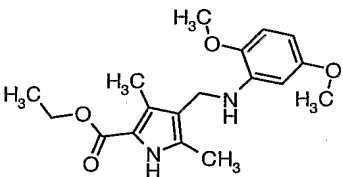
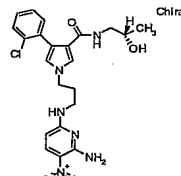
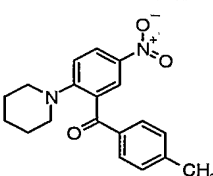
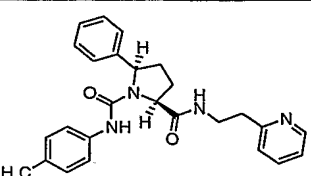
9		4-[(1-methyl-2-[[2-(methyloxy)phenyl]amino]-1H-benzimidazol-5-yl)oxy]-N-[3-(methyloxy)propyl]pyridine-2-carboxamide	462.5
10		4-({2-[(4-ethylphenyl)amino]-1,3-benzoxazol-5-yl}oxy)-N-methylpyridine-2-carboxamide	389.4
11		1-[(3-fluorophenyl)carbonyl]-4-[[4-(trifluoromethyl)phenyl]methyl]piperazine	367.4
12		1-[2-(ethyloxy)phenyl]-4-[[3,4,5-tris(methyloxy)phenyl]carbonyl]piperazine	401.5
13		1-(3-chlorophenyl)-4-[[2-(ethyloxy)phenyl]carbonyl]piperazine	345.8
14		3-({4-[(2E)-3-phenylprop-2-enyl]piperazin-1-yl}carbonyl)-7-oxabicyclo[2.2.1]heptane-2-carboxylic acid	371.4
15		1-[2-(methyloxy)phenyl]-4-[[3,4,5-tris(methyloxy)phenyl]carbonyl]piperazine	387.4
16		3-[(4-pyridin-2-yl)piperazin-1-yl]carbonyl]-7-oxabicyclo[2.2.1]heptane-2-carboxylic acid	332.4

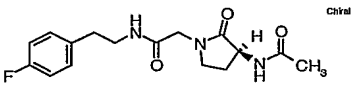
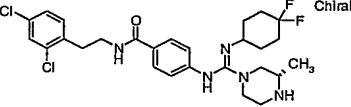
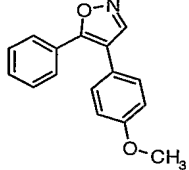
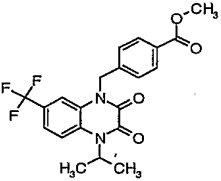
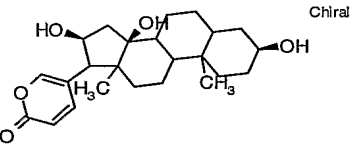
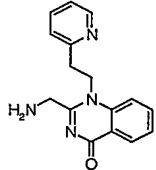
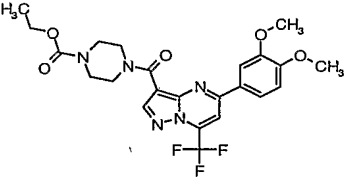
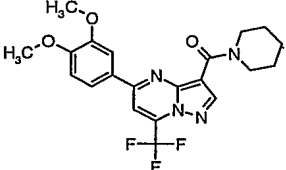
17		3-pentyl-7-[(4-phenyl)piperazin-1-yl]carbonyl]-2-thioxo-2,3-dihydroquinazolin-4(1H)-one	437.6
18		1-[(E)-({4-[(2,4-dimethylphenyl)methyl]piperazin-1-yl}imino)methyl]naphthalen-2-ol	374.5
19		5-chloro-1-[[3-(trifluoromethyl)phenyl]methyl]-1H-indole-2,3-dione	340.7
20		1-[(4-methylphenyl)methyl]-5-nitro-1H-indole-2,3-dione	297.3
21		1-methyl-6,7-bis(methoxy)-2-[[3-(methoxy)phenyl]carbonyl]-1,2,3,4-tetrahydroisoquinoline	342.4
22		1-methyl-6,7-bis(methoxy)-2-(naphthalen-2-ylcarbonyl)-1,2,3,4-tetrahydroisoquinoline	362.4
23		[2-(trifluoromethyl)phenyl]methyl 3-[4-(aminocarbonyl)phenyl]-2-cycloheptyl-1-oxo-1,2,3,4-tetrahydroisoquinoline-4-carboxylate	565.6
24		anthra[1,2-c][1,2,5]thiadiazole-6,11-dione	267.3

25		benzo[b]oxanthrene-6,11-dione	265.2
26		ethyl 6,11-dioxo-6,11-dihydrobenzo[b]phenazine-2-carboxylate	333.3
27		N,N-dimethyl-9,10-dioxo-9,10-dihydroanthracene-1-sulfonamide	316.3
28		2-(trifluoromethyl)-3-[[3,4,5-tris(methoxy)phenyl]carbonyl]naphtho[2,3-b]furan-4,9-dione	461.4
29		2-(2-oxopropyl)-2-phenyl-1H-indene-1,3(2H)-dione	279.3
30		ethyl 4-{5-[(3-nitrophenyl)carbonyl]-1,3-dioxo-1,3-dihydro-2H-isoindol-2-yl}benzoate	445.4
31		5,6-dichloro-2-[2-chloro-5-(trifluoromethyl)phenyl]-1H-isoindole-1,3(2H)-dione	395.6
32		3-bromo-4-[[[2-fluorophenyl)methyl]oxy]-5-(methoxy)benzaldehyde thiosemicarbazone	413.3

33		2-[4-(3-chlorophenyl)piperazin-1-yl]-5-nitrobenzaldehyde thiosemicarbazone	419.9
34		4-[[2-(3-chlorophenyl)ethyl]amino]-3-nitrobenzaldehyde thiosemicarbazone	378.9
35		(1E)-6,9-dimethyl-2,3,4,9-tetrahydro-1H-carbazol-1-one thiosemicarbazone	287.4
36		(2E)-1,1'-bi(cyclohexan)-1-en-2-one thiosemicarbazone	252.4
37		4-[[2-(4-chlorophenyl)ethyl]amino]-3-nitrobenzaldehyde thiosemicarbazone	378.9
38		4-(diethylamino)-2-[[4-(4-fluorophenyl)methyl]oxy]benzaldehyde N-(2-piperidin-1-ylethyl)thiosemicarbazone	486.7
39		3,4-bis(methoxy)benzaldehyde (1,1-dioxido-1,2-benzisothiazol-3-yl)(methyl)hydrazone	360.4
40		(2E)-2-[(4-chlorophenyl)(5-chlorothiophen-2-yl)methylidene]hydrazinecarboximidamide	314.2

41		2-(4-amino-2-oxo-1-propyl-1,2-dihydroquinolin-3-yl)-1H-benzimidazole-6-carbonitrile	344.4
42		4-amino-6-fluoro-7-({[4-(methoxy)phenyl]methyl}amino)-3-[5-(4-methylpiperazin-1-yl)-1H-benzimidazol-2-yl]quinolin-2(1H)-one	528.6
43		6-chloro-3-(5-chloro-1H-benzimidazol-2-yl)-4-{{2-(dimethylamino)ethyl}amino}quinolin-2(1H)-one	417.3
44		4-amino-5-(1H-benzimidazol-2-yl)-1-methyl-1,7-dihydro-6H-pyrazolo[3,4-b]pyridin-6-one	281.3
45		5,5-dimethyl-4-methylidene-3-(2,4,6-trinitrophenyl)-1,3-oxazolidin-2-one	339.2
46		5-methyl-2-[4-(methoxy)phenyl]hexahydro-1H-isoindole-1,3(2H)-dione	274.3
47		5-methyl-2-(4-methylphenyl)hexahydro-1H-isoindole-1,3(2H)-dione	258.3
48		N~2~-(4-chlorophenyl)-6,6-dimethyl-1,6-dihydro-1,3,5-triazine-2,4-diamine	252.7

49		(7Z)-7-(furan-2-ylmethylidene)-3-phenyl-3,4-dihydro-2H-[1,3]thiazolo[3,2-a][1,3,5]triazin-6(7H)-one	312.4
50		(3aR,9R,9aR)-6,7-dihydroxy-9-[3,4,5-tris(methoxy)phenyl]-3a,4,9,9a-tetrahydronaphtho[2,3-c]furan-1(3H)-one	387.4
51		6-chloro-2-(ethyloxy)-4-methyl-3-(4-nitrophenyl)-3a,4,9,9a-tetrahydro-3H-pyrrolo[2,3-b]quinoxaline	387.8
52		ethyl 2-(ethyloxy)-4-methyl-3a,4,9,9a-tetrahydro-3H-pyrrolo[2,3-b]quinoxaline-3-carboxylate	304.4
53		ethyl 4-([2,5-bis(methoxy)phenyl]amino)met hyl-3,5-dimethyl-1H-pyrrole-2-carboxylate	333.4
54		1-{3-[(6-amino-5-nitropyridin-2-yl)amino]propyl}-4-(2-chlorophenyl)-N-[(2S)-2-hydroxypropyl]-1H-pyrrole-3-carboxamide	473.9
55		(4-methylphenyl)(5-nitro-2-piperidin-1-ylphenyl)methanone	325.4
56		(2S,5R)-N~1~-(4-methylphenyl)-5-phenyl-N~2~-(2-pyridin-2-ylethyl)pyrrolidine-1,2-dicarboxamide	429.5

57		2-[(3S)-3-(acetylamino)-2-oxopyrrolidin-1-yl]-N-[2-(4-fluorophenyl)ethyl]acetamide	322.4
58		N-[2-(2,4-dichlorophenyl)ethyl]-4-({(Z)-[(4,4-difluorocyclohexyl)imino][(3S)-3-methylpiperazin-1-yl]methyl}amino)benzamide	553.5
59		4-[4-(methyloxy)phenyl]-5-phenylisoxazole	252.3
60		methyl 4-[[4-(1-methylethyl)-2,3-dioxo-7-(trifluoromethyl)-3,4-dihydroquinoxalin-1(2H)-yl]methyl]benzoate	421.4
61		(3beta,16beta)-3,14,16-trihydroxybufa-20,22-dienolide	403.5
62		2-(aminomethyl)-1-(2-pyridin-2-ylethyl)quinazolin-4(1H)-one	281.3
63		ethyl 4-[[5-[3,4-bis(methyloxy)phenyl]-7-(trifluoromethyl)pyrazolo[1,5-a]pyrimidin-3-yl]carbonyl]piperazine-1-carboxylate	508.5
64		5-[3,4-bis(methyloxy)phenyl]-3-(piperidin-1-ylcarbonyl)-7-(trifluoromethyl)pyrazolo[1,5-a]pyrimidine	435.4

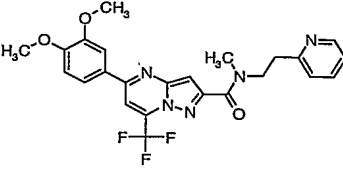
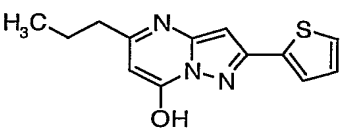
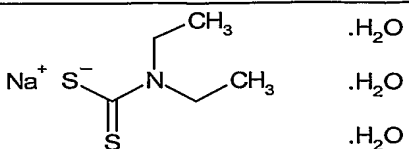
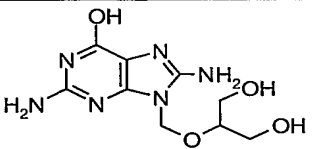
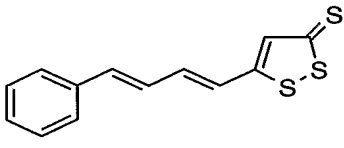
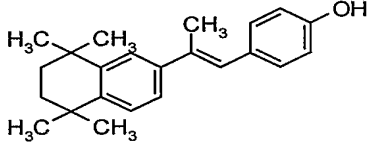
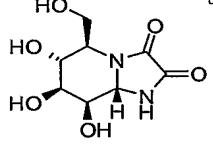
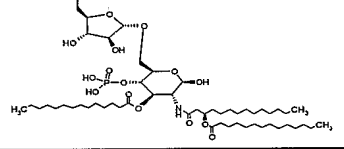
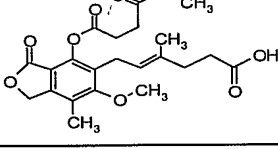
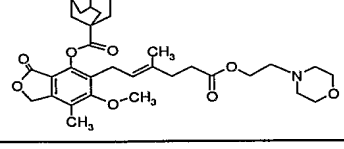
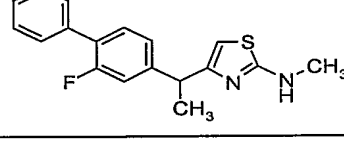
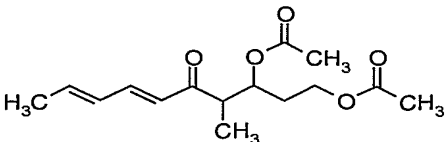
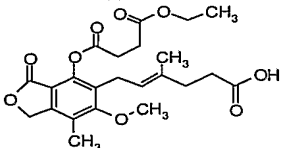
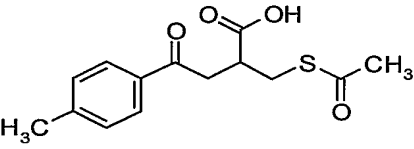
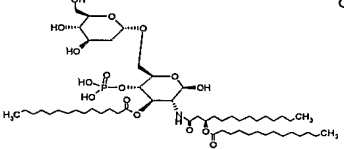
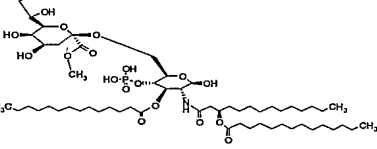
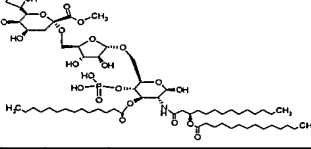
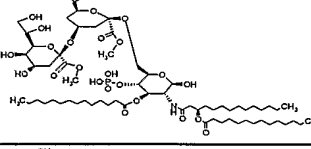
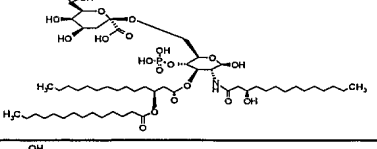
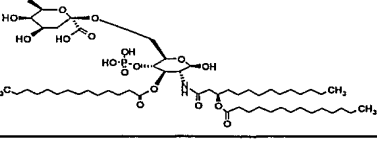
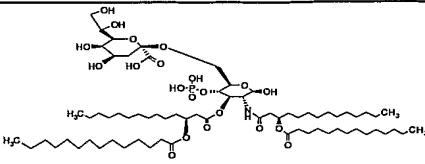
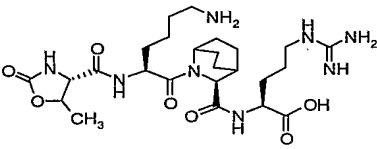
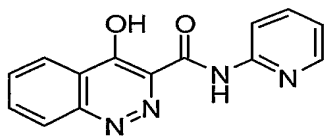
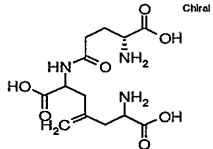
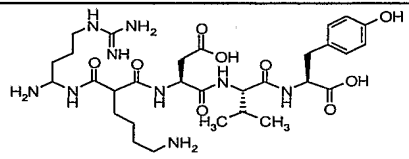
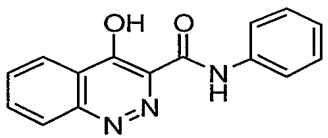
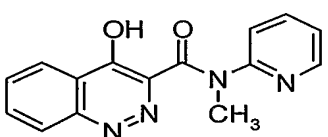
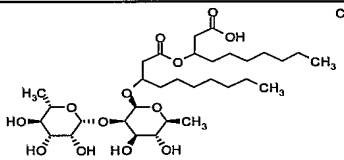
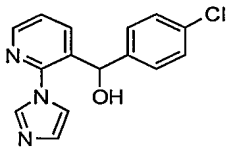
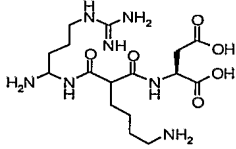
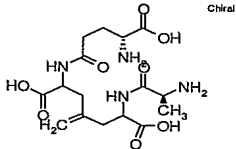
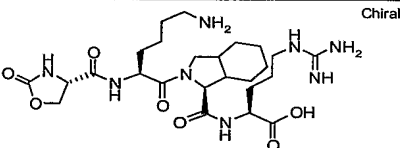
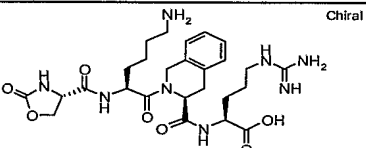
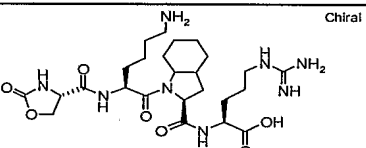
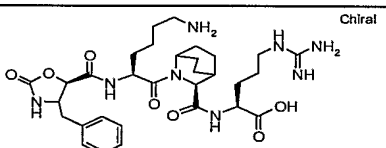
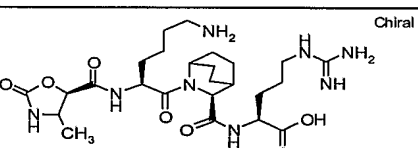
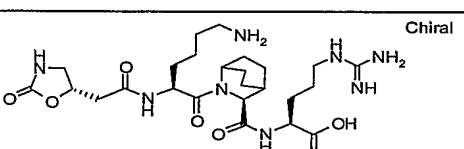
65		5-[3,4-bis(methoxy)phenyl]-N-methyl-N-(2-pyridin-2-ylethyl)-7-(trifluoromethyl)pyrazolo[1,5-a]pyrimidine-2-carboxamide	486.5
66		5-propyl-2-thien-2-ylpyrazolo[1,5-a]pyrimidin-7-ol	260.3

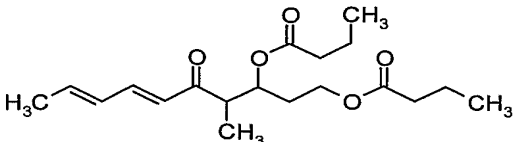
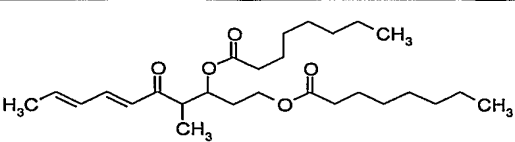
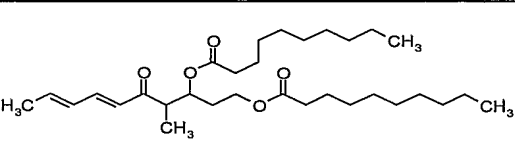
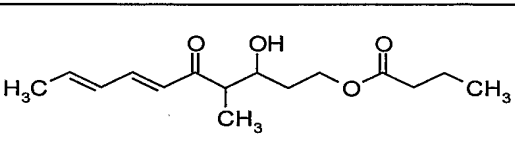
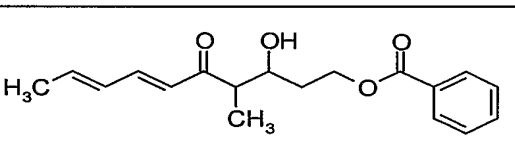
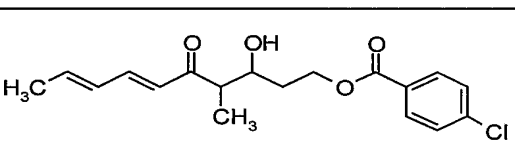
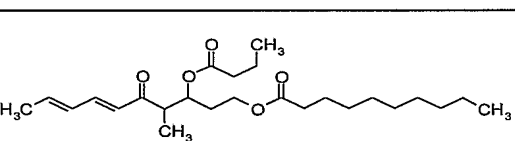
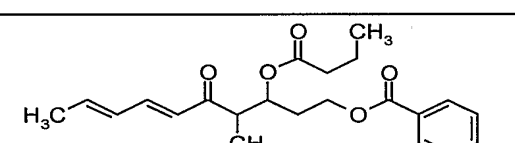
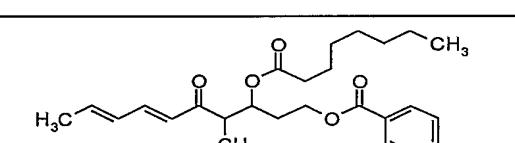
Table 35

Compound #	Structure	Source	Literature Reference	Patent Number
1		Aventis Pasteur	1) Lang, J.-M.; Touraine, J.-L.; Trepo, C. et al. Lancet 1988, 2(8613): 702-5.	
2		Pfizer	Dong, M.K. et al. Pharmacologist 1988, 30(3): Abst 87.8.	ES 8602792
3		Mitsui Chemicals	Mizuno, O. et al. 4th Int Conf Immunopharmacol (May 15-19, Osaka) 1988, Abst WS6-3.	EP 236929
4		Roche		EP 407788
5		Fujisawa	1) Iwami, M. et al. J Antibiot 1987, 40(5): 612-22.	JP 87161796
6		Novartis		FR 2604177
7		Roche Bioscience		US 4725622
8		Roche Bioscience		US 4727069
9		Sumitomo	1) Nishikaku, F. and Koga, Y. 4th Int Conf Immunopharmacol (May 15-19, Osaka) 1988, Abst WS6-8.	EP 248399

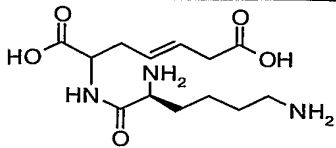
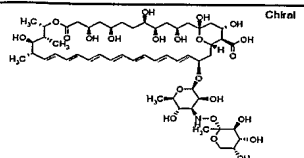
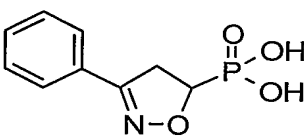
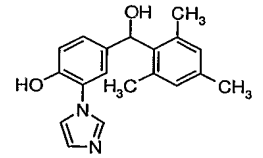
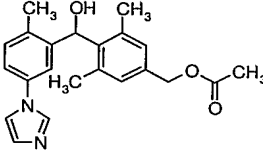
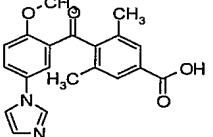
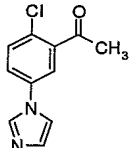
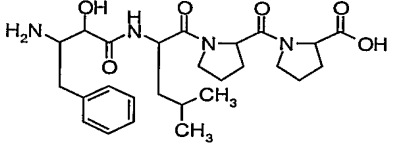
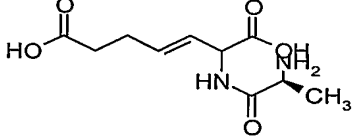
10		SSP		JP 88022053
11		Roche Bioscience		US 4725622
12		Taisho	1) Kameo, K. et al. Chem Pharm Bull 1988, 36(6): 2050-60.	EP 164101
13	 Chiral	Novartis		FR 2604177
14	 Chiral	Novartis		FR 2604177
15	 Chiral	Novartis		FR 2604177
16	 Chiral	Novartis		FR 2604177
17	 Chiral	Novartis		FR 2604177
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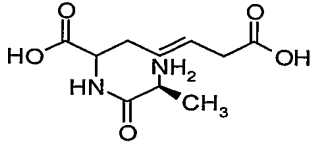
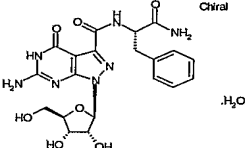
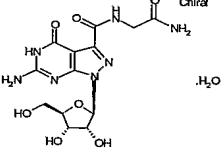
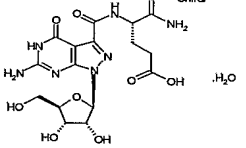
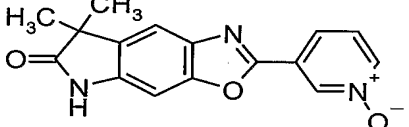
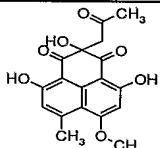
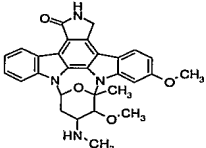
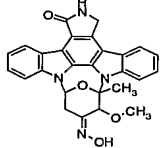
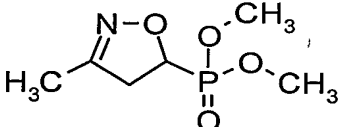
19	 Chiral	Novartis		FR 2604177
20	 Chiral	ADIR		AU 8811669
21		Pharmacia		AU 8810908
22	 Chiral	Aventis Pharma		EP 284461
23		Eniricerche		EP 282891
24		Pharmacia		AU 8810908
25		Pharmacia		AU 8810908
26	 Chiral	Abbott	Swanson, R.N. et al. 28th Intersci Conf Antimicrob Agents Chemother (Oct 23-26, Los Angeles) 1988, Abst 972 .	
27		Mitsubishi Pharma		JP 88119425

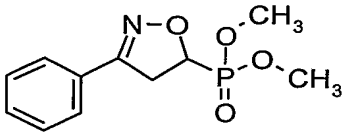
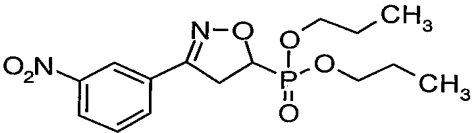
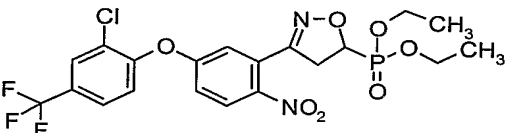
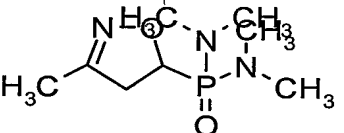
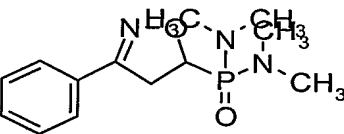
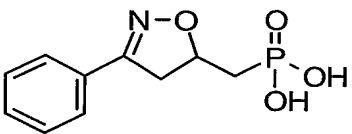
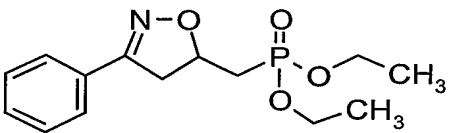
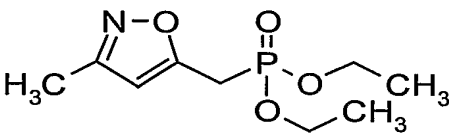
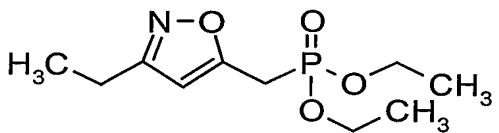
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29		Eniricerche	EP 282891
30	<p>Chiral</p> 	Aventis Pharma	EP 284461
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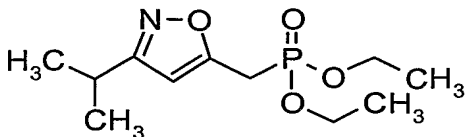
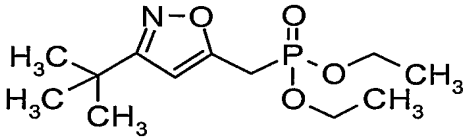
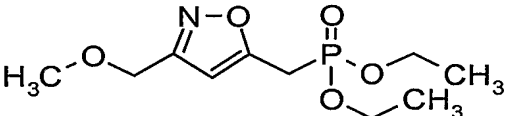
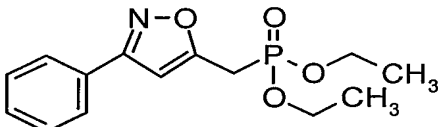
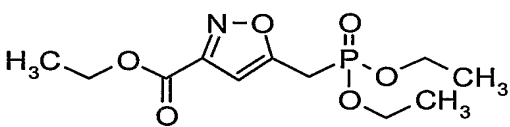
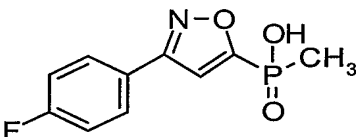
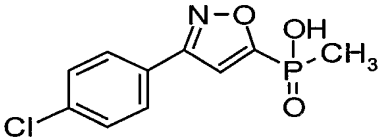
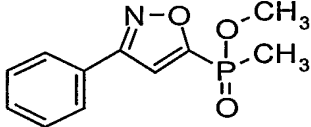
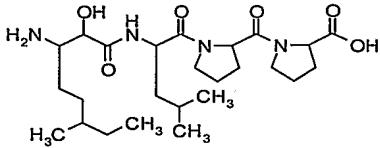
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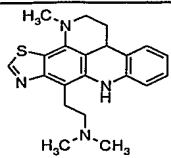
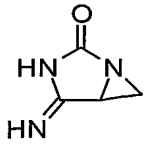
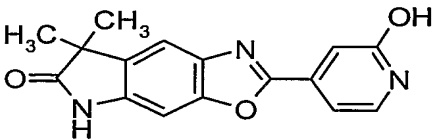
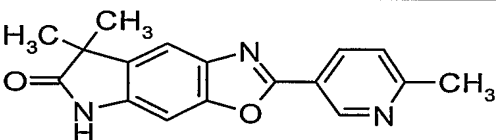
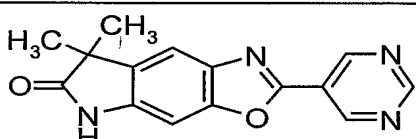
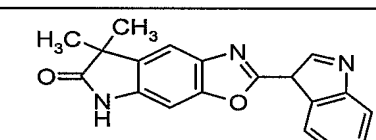
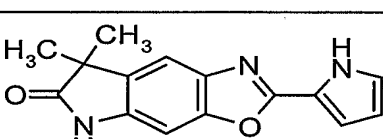
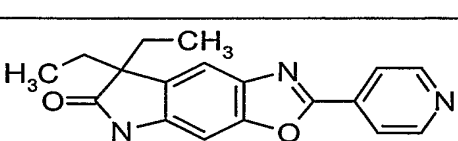
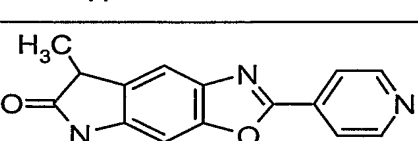
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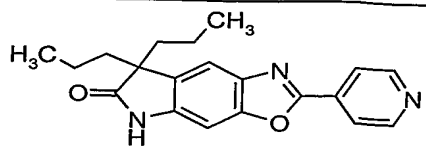
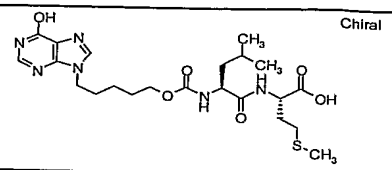
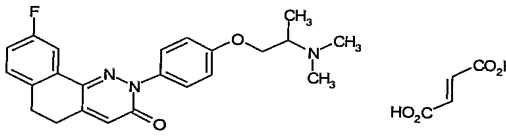
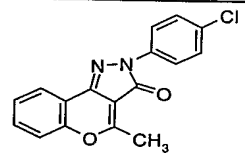
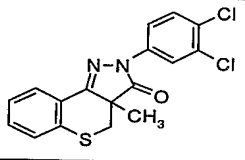
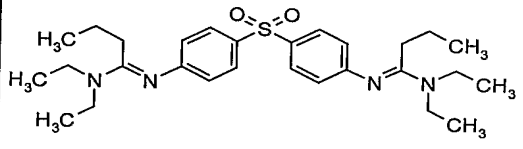
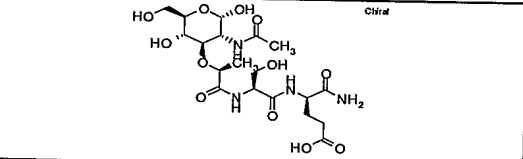
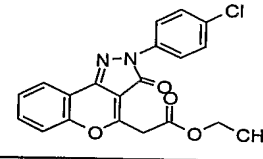
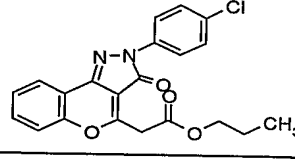
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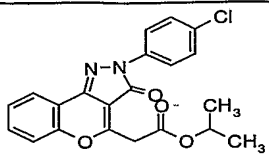
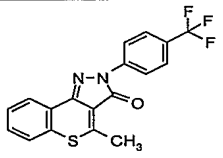
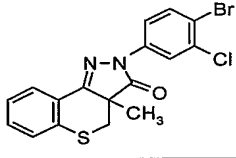
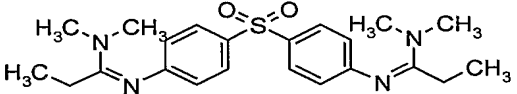
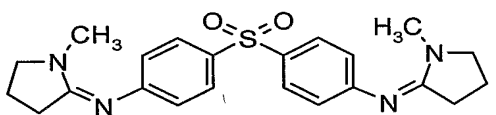
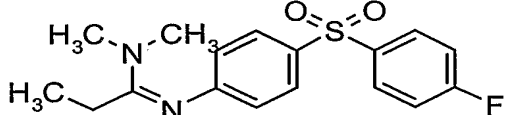
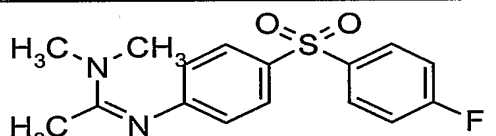
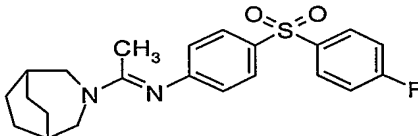
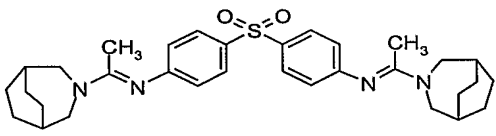
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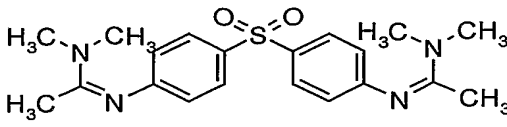
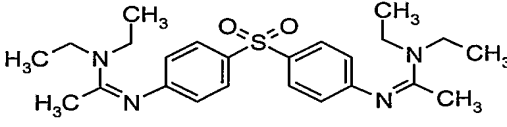
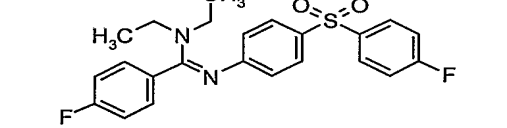
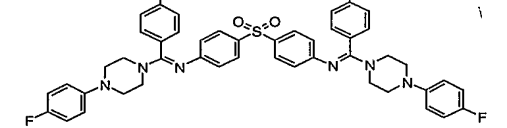
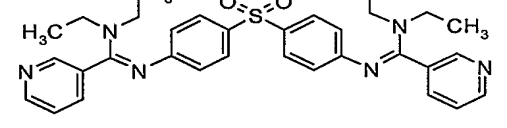
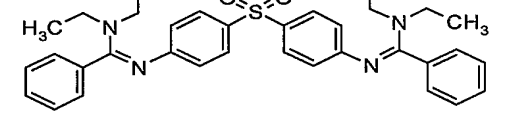
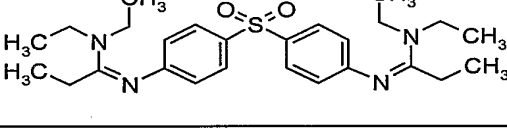
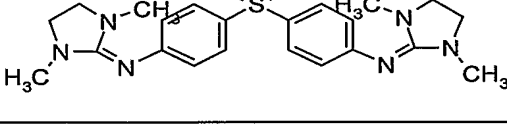
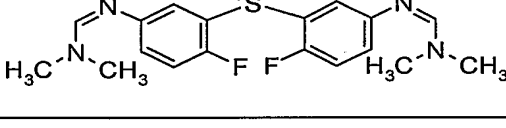
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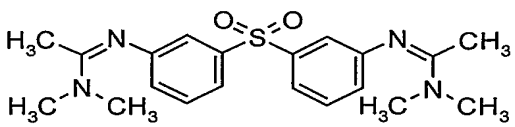
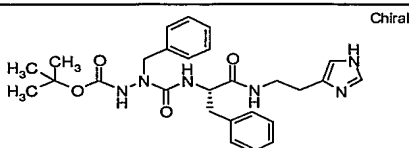
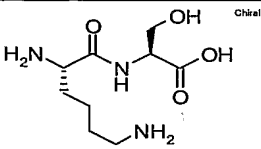
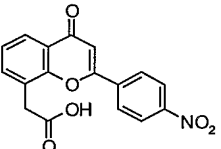
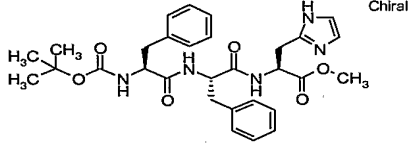
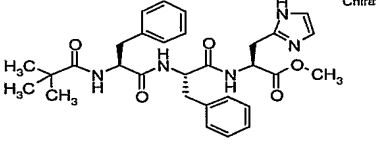
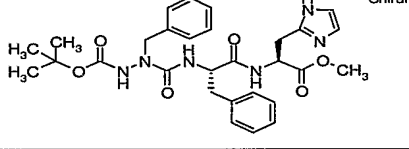
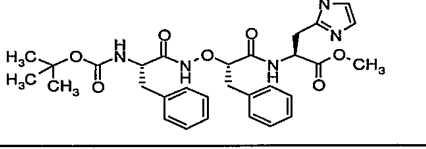
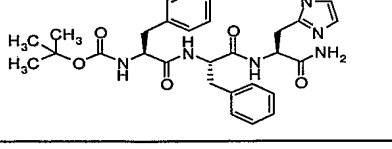
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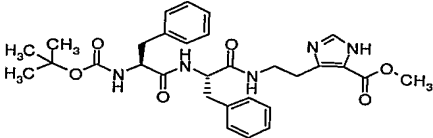
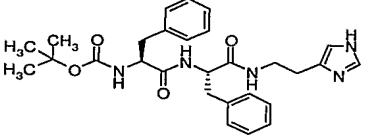
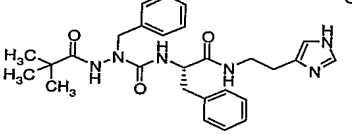
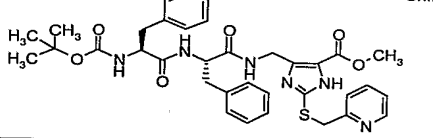
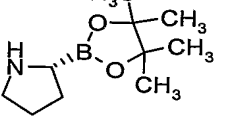
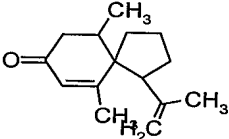
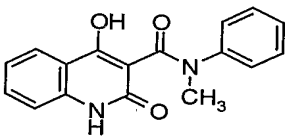
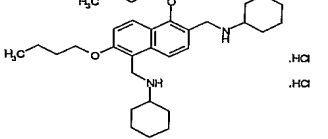
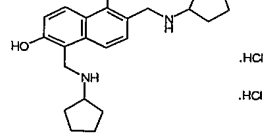
91		Harbor Branch Oceanographic Institution		EP 331320
92		Roche	1) Herrmann, D.B.J. 17th Int Cong Chemother (June 23-28, Berlin) 1991, Abst 838 .	EP 352652
93		Roche		AU 8931653
94		Roche		AU 8931653
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101	 Chiral	Roche		AU 8931653
102		Scharper	1) Migliorati, G. et al. 7th Int Cong Immunol (July 30-Aug 5, Berlin) 1989, Abst 106-62 .	
103		Mitsubishi Pharma		EP 351435
104		Abbott GmbH		EP 354693
105		Abbott GmbH		EP 354694
106	 Chiral	Wyeth		EP 354303
107		Merck & Co.		US 4866035
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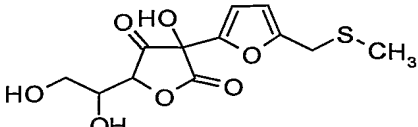
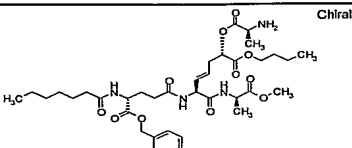
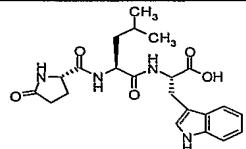
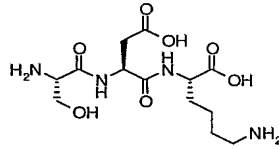
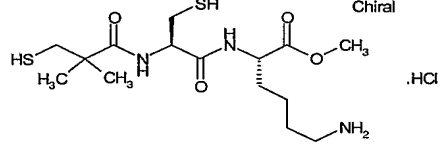
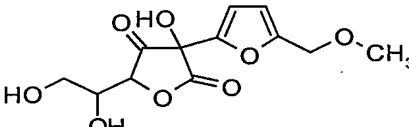
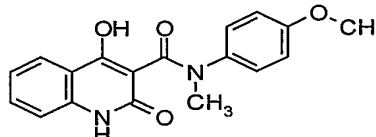
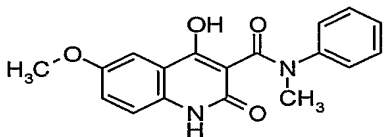
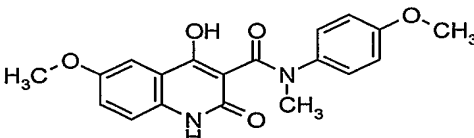
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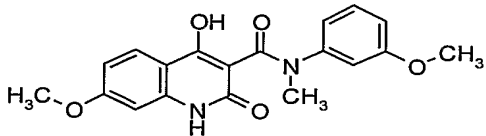
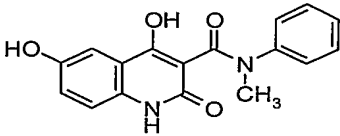
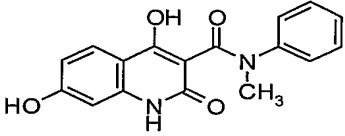
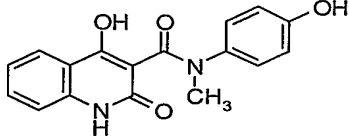
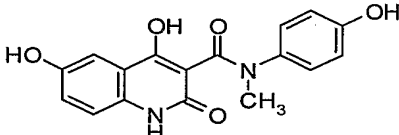
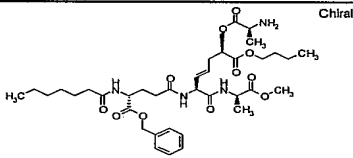
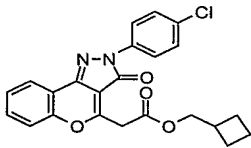
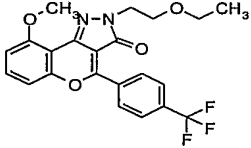
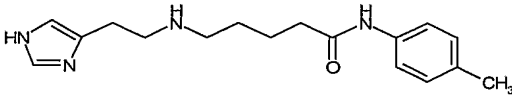
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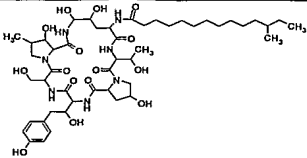
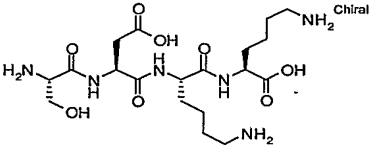
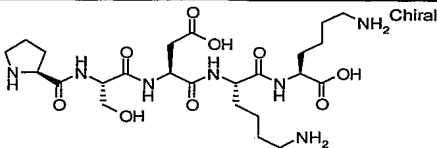
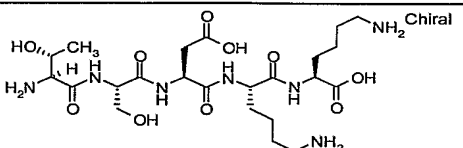
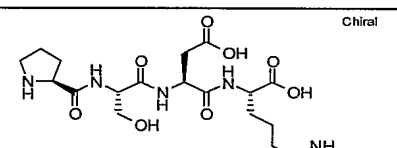
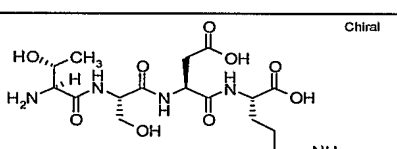
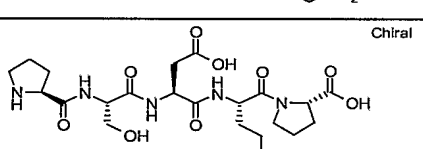
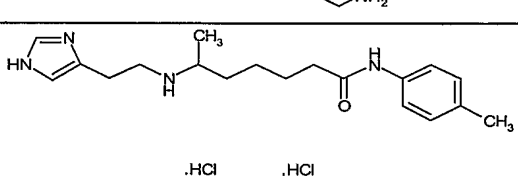
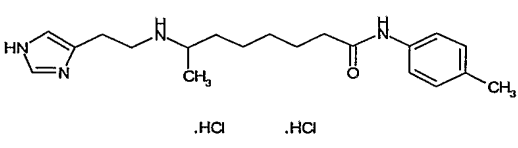
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128	 Chiral	Tanabe		EP 372818
129	 Chiral	Elan	1) Eldon, M.A. et al. J Clin Pharmacol 1990, 30(4): 352-7.	
130		Lipha		EP 341104
131	 Chiral	Tanabe		EP 372818
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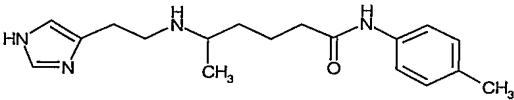
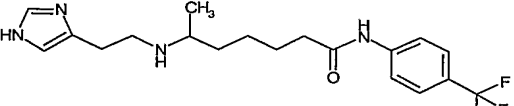
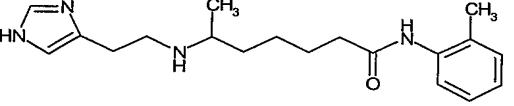
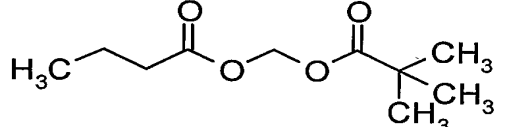
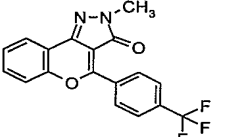
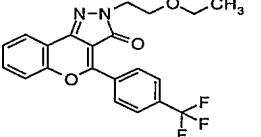
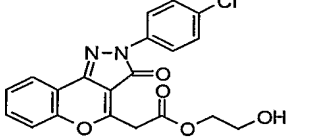
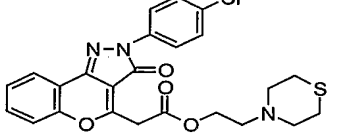
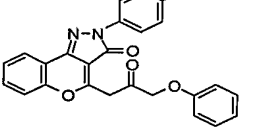
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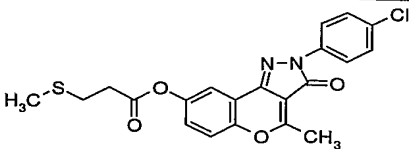
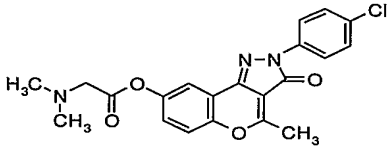
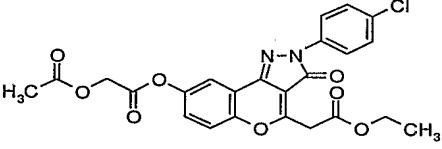
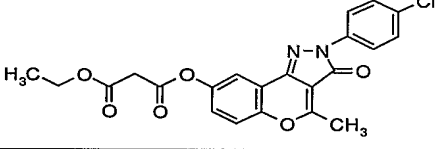
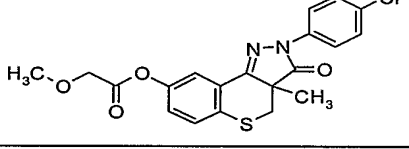
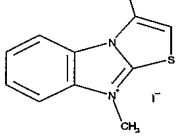
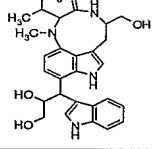
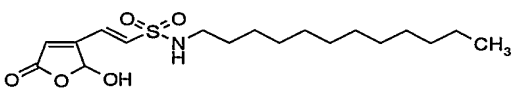
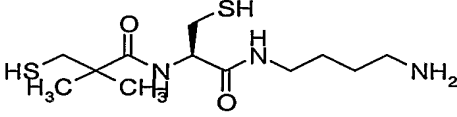
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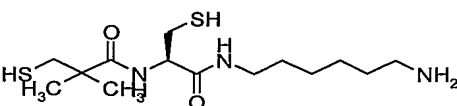
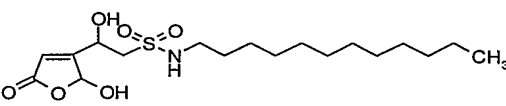
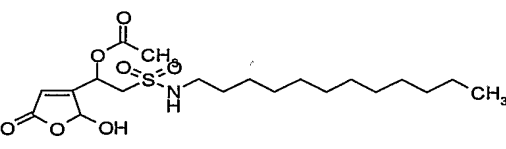
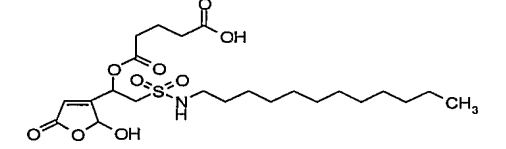
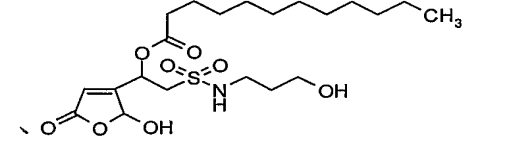
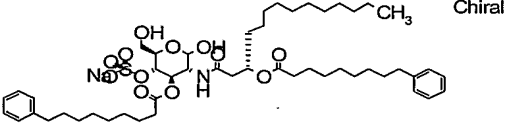
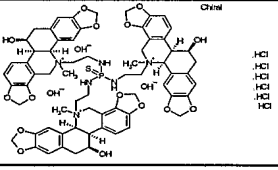
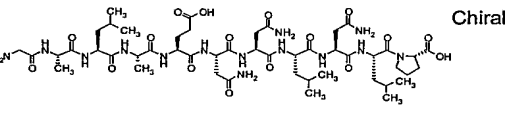
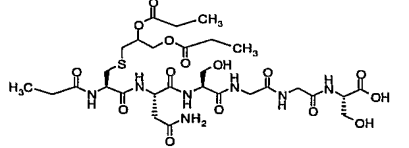
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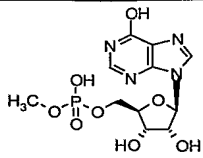
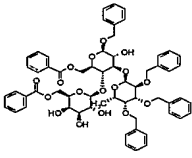
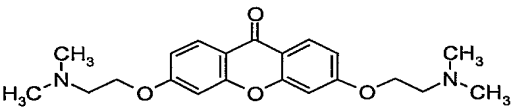
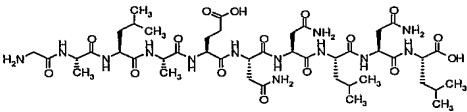
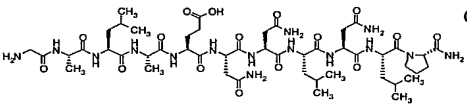
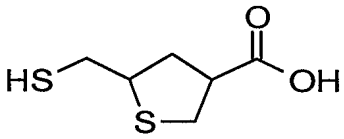
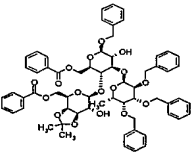
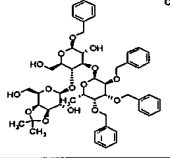
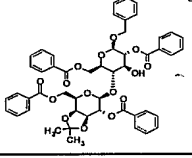
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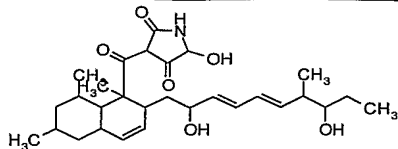
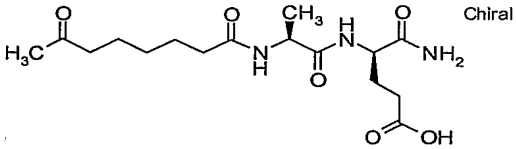
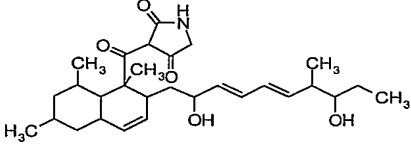
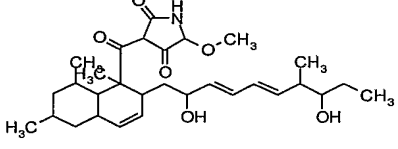
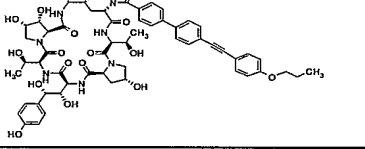
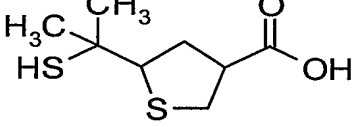
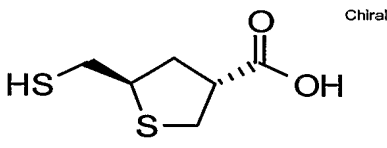
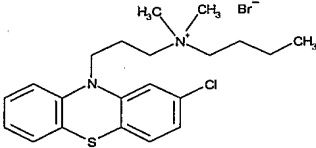
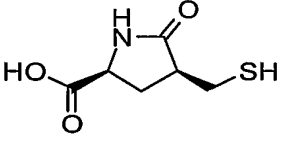
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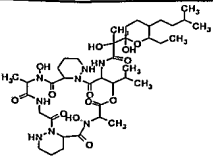
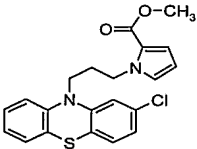
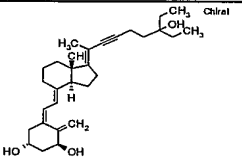
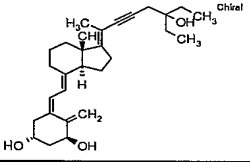
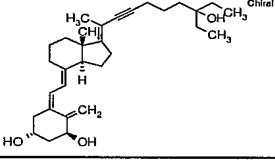
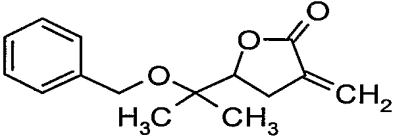
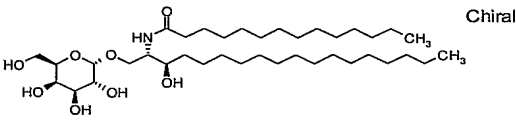
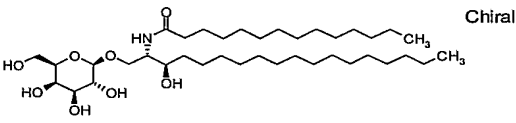
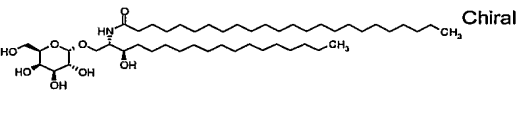
181	 <chem>CC1=CC=C(NC1CCNC(C)CCCCC(=O)Nc2ccc(C)cc2)C3=CC=CC=N3</chem> .HCl .HCl	Leland Stanford Junior University		US 4996221
182	 <chem>CC1=CC=C(NC1CCNC(C)CCCCC(=O)Nc2ccc(C(F)(F)F)cc2)C3=CC=CC=N3</chem> .HCl .HCl	Leland Stanford Junior University		US 4996221
183	 <chem>CC1=CC=C(NC1CCNC(C)CCCCC(=O)Nc2ccccc2C)C3=CC=CC=N3</chem> .HCl .HCl	Leland Stanford Junior University		US 4996221
184	 <chem>CC(C)(C)C(=O)OCOC(=O)CCCC=O</chem>	Bar-Ilan University	1) Rephaeli, A. et al. Int J Cancer 1991, 49(1): 66.	EP 302349
185	 <chem>CC1=CC=C(NC1CC2=CC=CC=C2O3C(=O)N(C)N=C3C2c4ccc(C(F)(F)F)cc4)C5=CC=CC=C5</chem>	Abbott GmbH		WO 9112255
186	 <chem>COCCOC1=CC=C(NC1CC2=CC=CC=C2O3C(=O)N(C)N=C3C2c4ccc(C(F)(F)F)cc4)C5=CC=CC=C5</chem>	Abbott GmbH		WO 9112255
187	 <chem>CCOC(=O)C1=CC=C(NC1CC2=CC=CC=C2O3C(=O)N(C)N=C3C2c4ccc(Cl)cc4)C5=CC=CC=C5</chem>	Abbott GmbH		WO 9111448
188	 <chem>C1CCN(CS1)CCOC(=O)C2=CC=C(NC2CC3=CC=CC=C3O4C(=O)N(C)N=C4C3c5ccc(Cl)cc5)C6=CC=CC=C6</chem>	Abbott GmbH		WO 9111448
189	 <chem>c1ccc(cc1)COC(=O)C2=CC=C(NC2CC3=CC=CC=C3O4C(=O)N(C)N=C4C3c5ccc(Cl)cc5)C6=CC=CC=C6</chem>	Abbott GmbH		WO 9111448

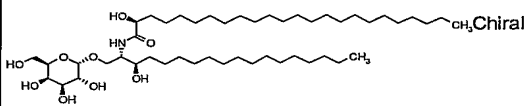
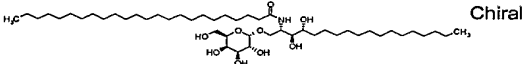
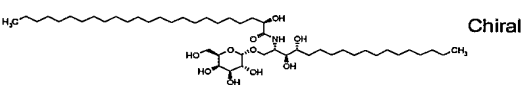
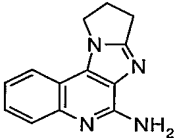
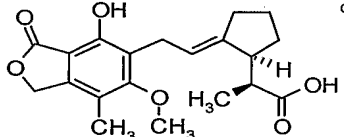
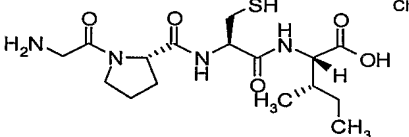
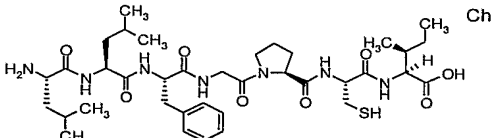
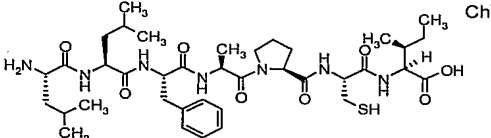
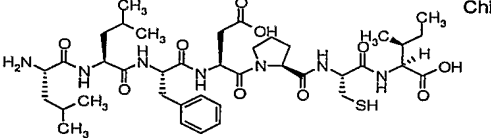
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195		Bashkir Medical University	Dianov, V.M. et al. Khim Farm Zh SSSR 1991, 25(1): 40.	
196		Microbial Chemistry Research Foundation	Kumagai, H. et al. J Antibiot 1991, 44(9): 1029.	
197		Allergan		US 5081261
198	 Chiral	Santen		EP 455833

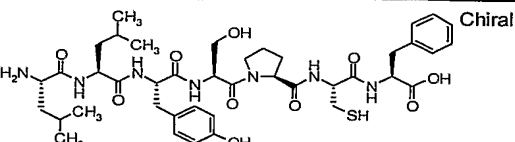
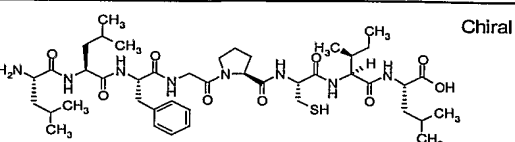
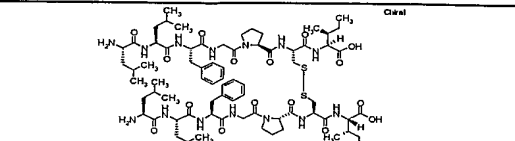
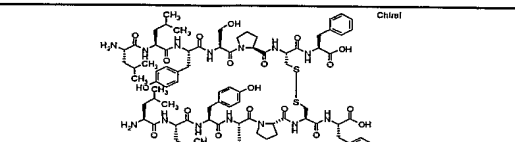
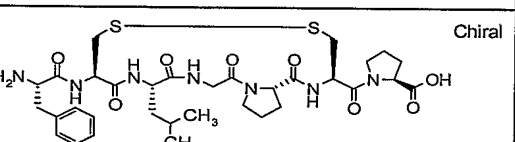
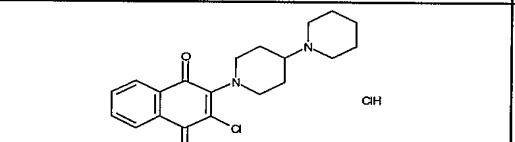
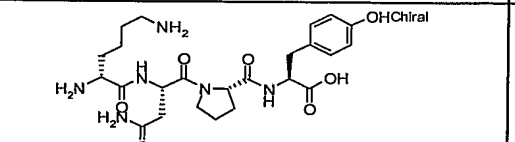
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204	 <p>Chiral</p>	Ono	1) Satoh, M. et al. 51st Annu Meet Jpn Cancer Assoc (Sept 29-Oct 1, Osaka) 1992, Abst 1450	EP 553786
205	 <p>Chiral</p>	Nowicky	1) Hohenwarter, O.; Strutzenberger, K.; Katinger, H.; Liepins, A.; Nowicky, J.W. Drug Exp Clin Res 1992, 18(Suppl.): 1.	WO 8300486
206	 <p>Chiral</p>	Tanabe		US 5210075
207		Fujisawa	1) Kurimura, M. et al. Pept Chem (1991) 1992, 361.	

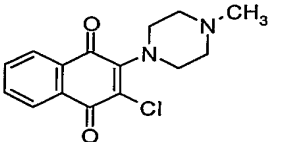
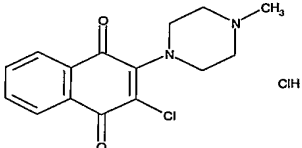
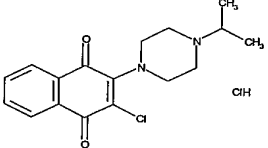
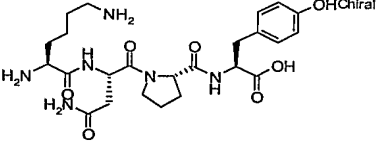
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210		Karolinska Institute	1) Algarra, I. et al. Int J Cancer 1993, 54: 518.	
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212		Tanabe		US 5210075
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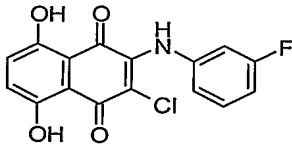
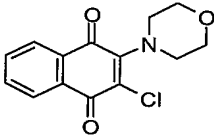
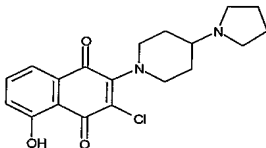
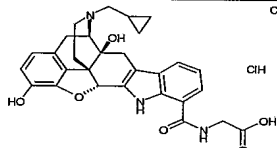
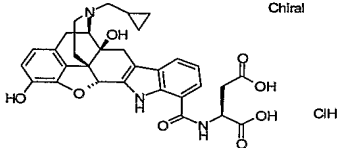
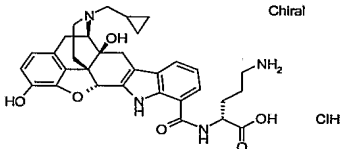
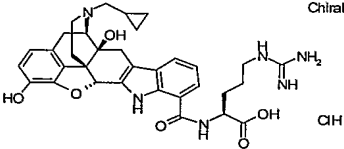
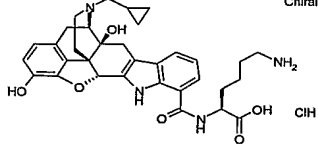
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220		Microbial Chemistry Research Foundation		
221		Lilly	1) Bartlett, M.S. et al. 33rd Intersci Conf Antimicrob Agents Chemother (Oct 17-20, New Orleans) 1993, Abst 369.	EP 561639
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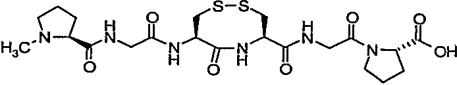
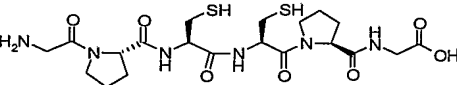
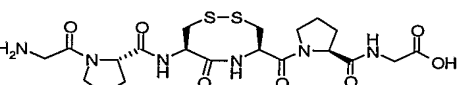
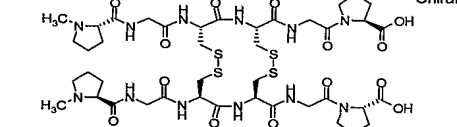
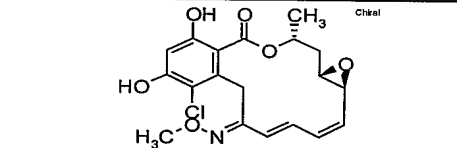
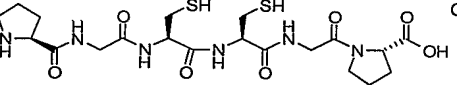
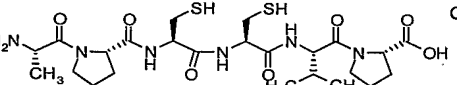
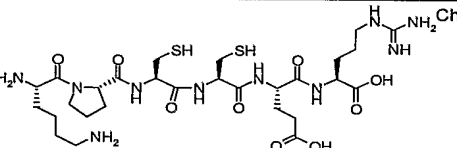
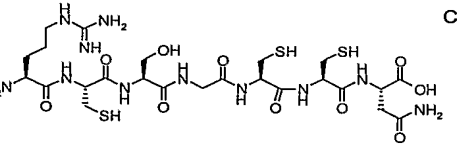
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232		Kirin Brewery	1) Morita, M. et al. J Med Chem 1995, 38(12): 2176.	1) EP 609437
233		Kirin Brewery		1) EP 609437
234		Kirin Brewery		1) EP 609437

235	 Chiral	Kirin Brewery		EP 609437
236	 Chiral	Kirin Brewery		EP 609437
237	 Chiral	Kirin Brewery		EP 609437
238		3M Pharmaceuticals	Lindstrom, K.J. et al. 211th ACS Natl Meet (March 24-28, New Orleans) 1996, Abst MEDI 210 .	US 5482936
239	 Chiral	Roche Bioscience	Smith, D.B. et al. J Org Chem 1996, 61(6): 2236.	WO 9522538
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249	$\begin{matrix} \text{Cys}^{\text{X1}} & \text{Thr} & \text{Lys} & \text{Pro} & \text{Arg} & \text{Glu} & \text{Gln} & \text{Gln} \\ \text{Gly} & \text{Cys}^{\text{X1}} & \text{Arg} & \text{Tyr} & \text{Thr} & \text{Ser} & \text{Asp} & \text{Tyr} & \text{Gln} \end{matrix}$	Peptech	WO 9612739
250	 OH	Japan Tobacco	JP 96113555
251	$\begin{matrix} \text{Leu} & \text{Pro} & \text{Lys} & \text{Pro} & \text{Pro} & \text{Lys} & \text{Pro} \\ \text{Ala} & \text{Met} & \text{Arg} & \text{Met} & \text{Lys} & \text{Ser} & \text{Val} \\ \text{Thr} & \text{Pro} & \text{Leu} & \text{Leu} & \text{Met} & \text{Glu} & \text{Ala} \\ & & & & \text{Met} & \text{Pro} & \text{Leu} \end{matrix}$	Harvard College	JP 96504177
252	 OHChiral	Shire BioChem	WO 9619494

253		Japan Tobacco	JP 96113555
254		Japan Tobacco	JP 96113555
255		Japan Tobacco	JP 96113555
256		Shire BioChem	WO 9619494
257	<p>Leu Pro Lys Pro Pro Lys Pro</p> <p>Ala Met Arg Met Lys Ser Val</p> <p>Thr Pro Leu Leu Met Glu Ala</p> <p>Gly Met Pro Leu</p>	Harvard College	JP 96504177
258	<p>Pro Lys Pro Pro Lys Pro</p> <p>Ala Met Arg Met Lys Ser Val</p> <p>Thr Pro Leu Leu Met Glu Ala</p> <p>Gly Met Pro Leu</p>	Harvard College	JP 96504177
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263		Japan Tobacco	JP 96113555
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271		AstraZeneca	WO 9630397
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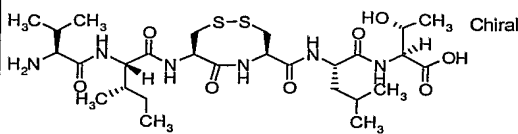
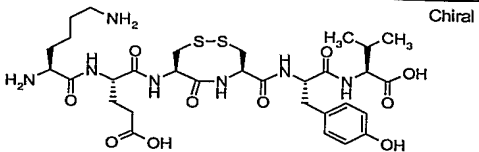
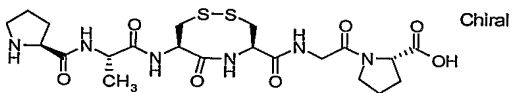
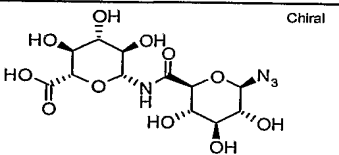
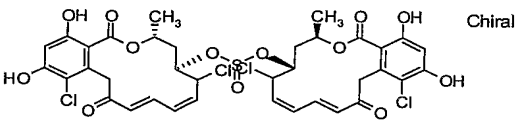
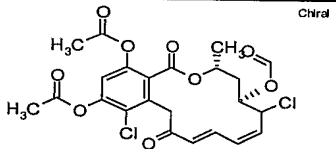
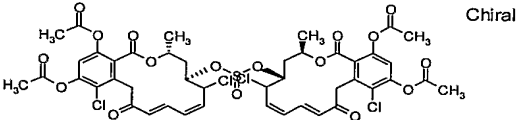
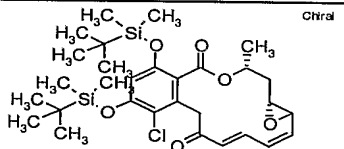
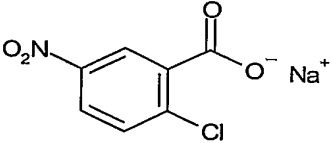
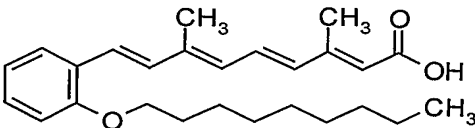
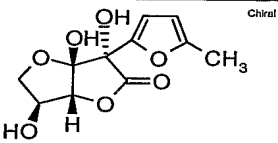
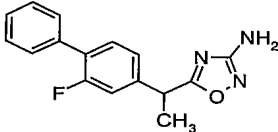
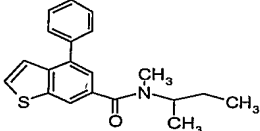
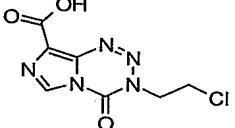
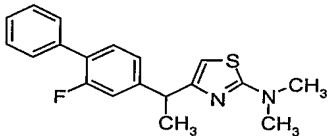
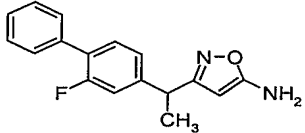
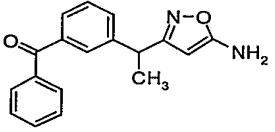
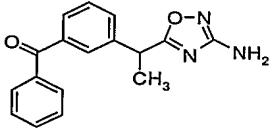
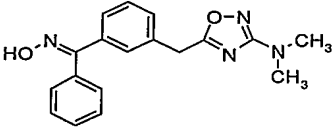
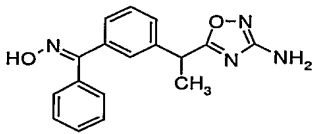
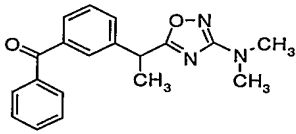
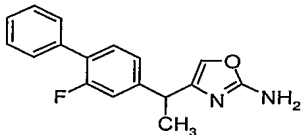
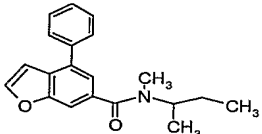
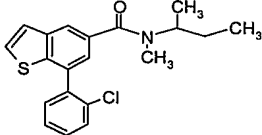
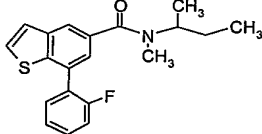
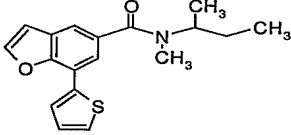
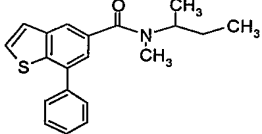
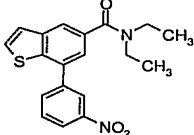
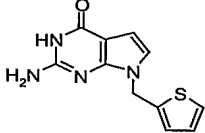
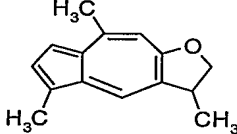
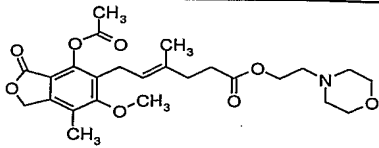
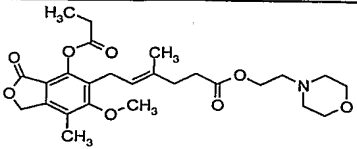
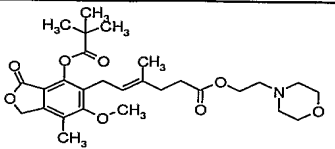
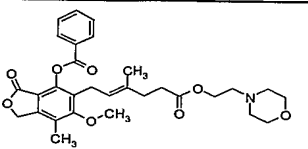
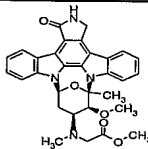
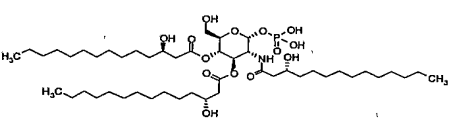
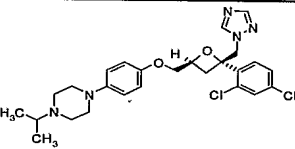
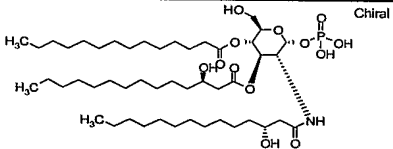
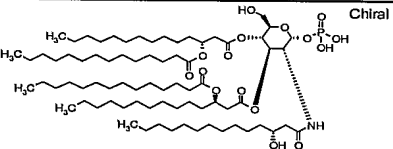
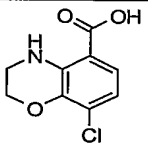

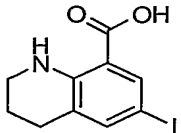
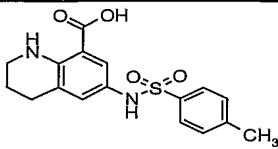
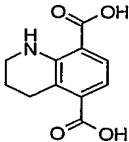
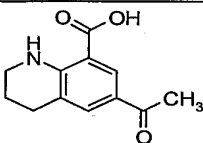
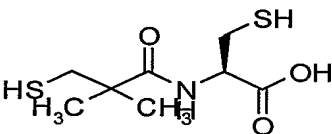
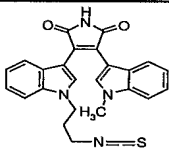
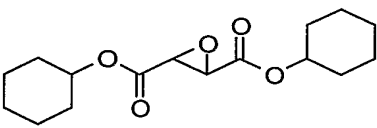
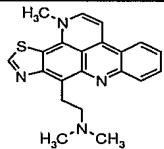
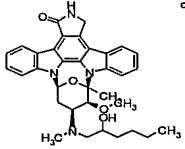
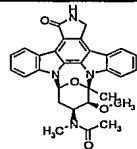
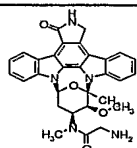
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283		Glycomed		WO 9635700
284		Kyowa Hakko		WO 9633989
285		Kyowa Hakko		WO 9633989
286		Kyowa Hakko		WO 9633989
287		Kyowa Hakko		WO 9633989
288		Aston University	Kinchington, D. et al. 4th Conf Retroviruses Opportunistic Infect (Jan 22-26, Washington DC) 1997, Abst .	

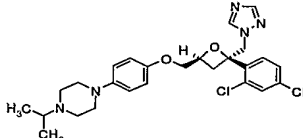
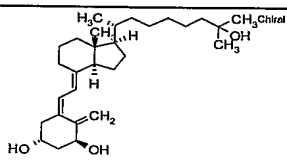

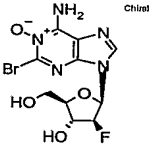

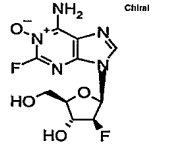
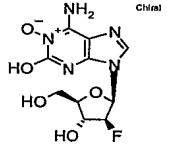
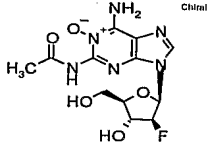
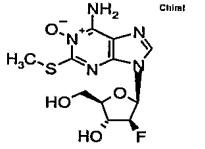
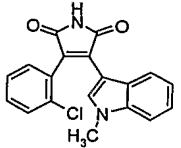
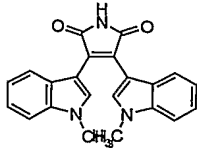
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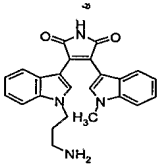
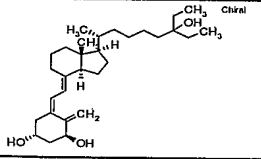
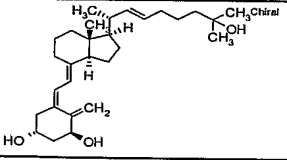
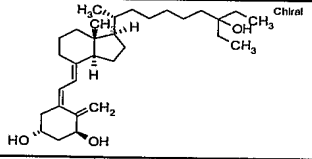
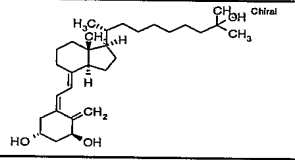
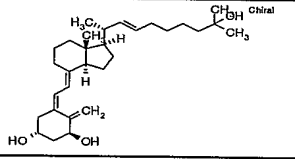
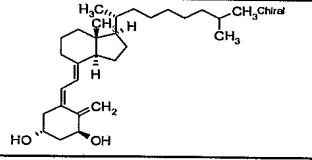
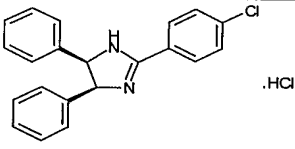
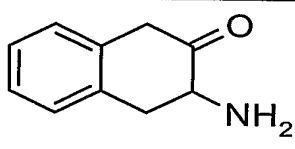
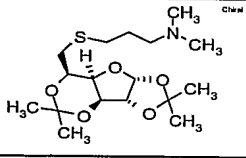
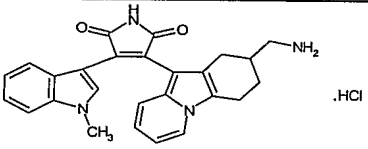
Compound #	Structure	Source	Literature Reference	Patent Number
289		Roche	1) Fiedler-Nagy, C. et al. Agent Action 1989, 27(3-4): 313-5.	EP 169571
290		NFCR	1) Forest Laboratories, Inc. Annual Report 1994.	WO 9517890
291		Sumitomo Pharmaceuticals		EP 248399
292		Aventis Pharma		EP 248734
293		May & Baker		EP 252682
294		Sumitomo Pharmaceuticals		EP 248399
295		Sumitomo Pharmaceuticals		EP 248399
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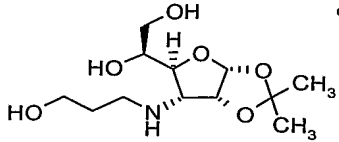
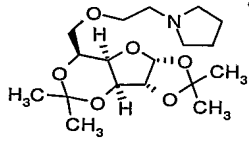
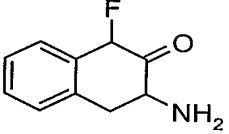
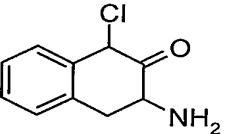
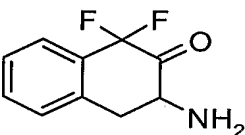
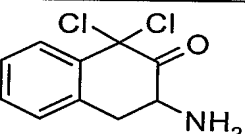
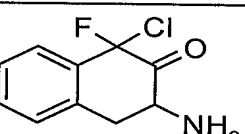
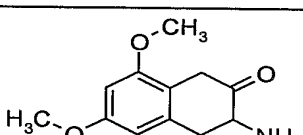
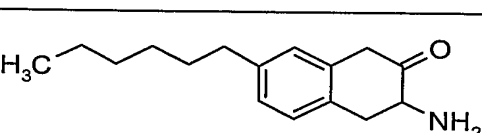
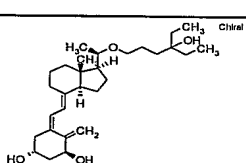
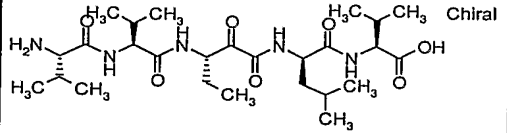
299		Sumitomo Pharmaceuticals		EP 248399
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307		Aventis Pharma		EP 248734
308		Pfizer		AU 8783281
309		Harbor Branch Found.		US 4755529

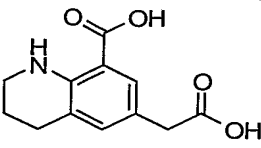
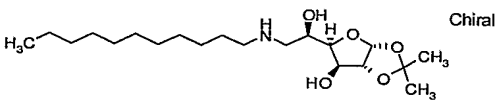
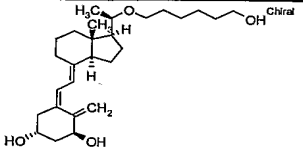
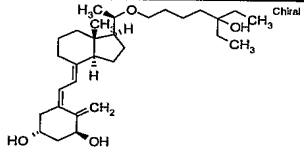
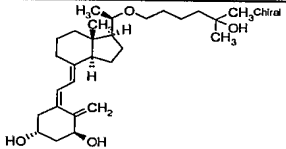
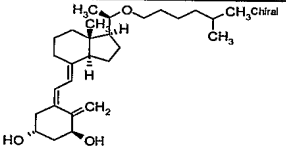
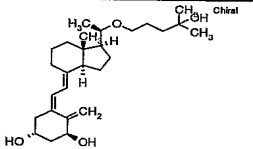
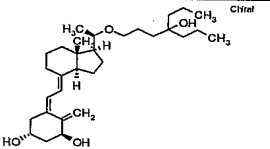
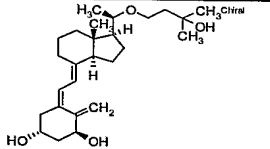
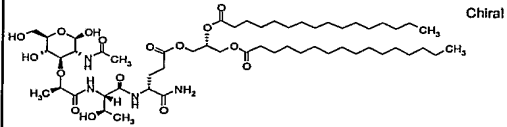
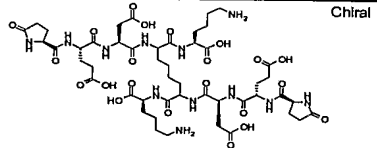
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312		Roche Bioscience		AU 8782540
313		Roche Bioscience		AU 8782540
314		Novartis		EP 296110
315		Novartis	1) Lam, C. et al. Antimicrob Agents Chemother 1991, 35(3): 500.	AU 8822785
316		Schering-Plough		EP 318214
317		Novartis		AU 8822785
318		Novartis		AU 8822785
319		Kyorin		EP 310096
320		Kyorin		EP 310096

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323		Kyorin		EP 310096
324		Kyorin		EP 310096
325		Santen		EP 326326
326		Roche		AU 8929658
327		Taisho	1) Takeshita, K. et al. Int J Immunother 1988, 4(2): 97-106.	JP 79141750
328		Harbor Branch Found.	1) Burres, N.S. et al. Proc Amer Assoc Cancer Res 1989, 30: Abst 1914.	EP 331320
329		Novartis		EP 296110
330		Novartis		EP 296110
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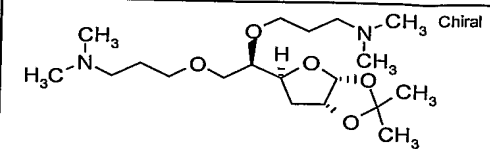
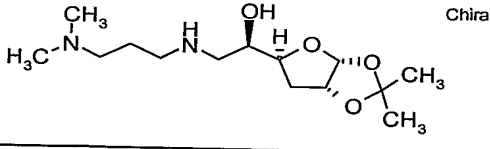
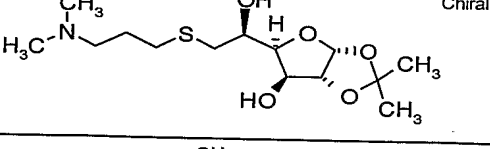
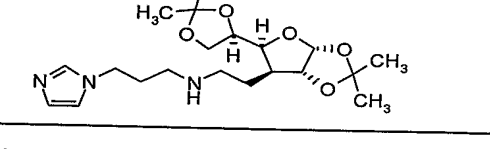
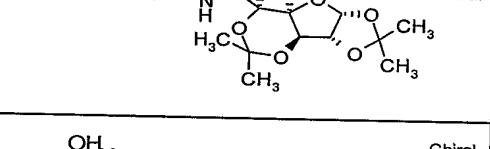
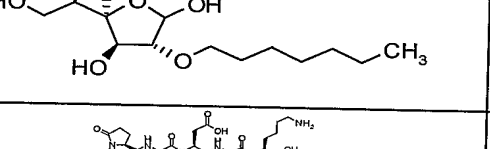
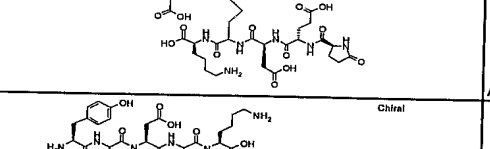
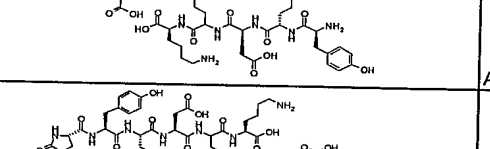
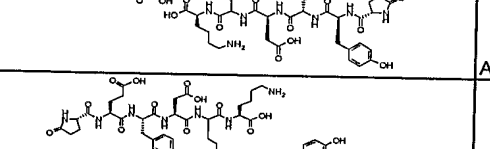
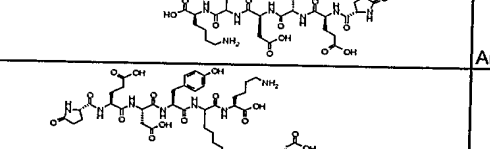
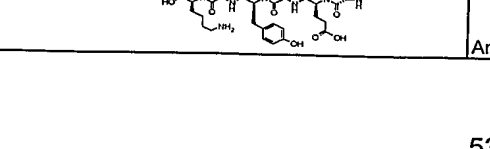
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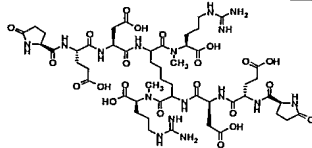
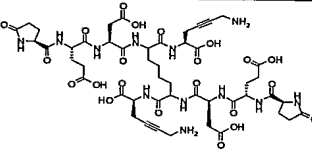
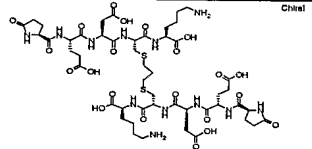
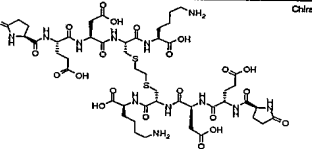
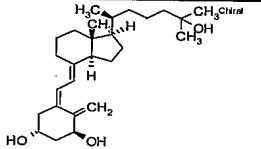
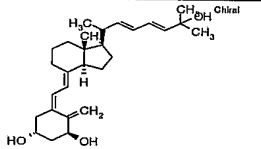
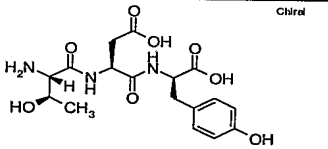
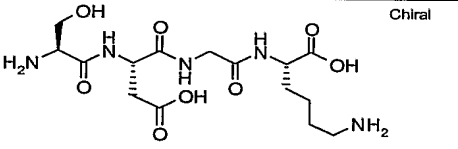
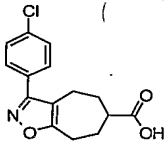
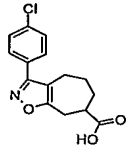
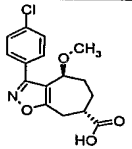
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350	 .HCl	Tanabe Seiyaku	1) Ueno, M. et al. Jpn J Pharmacol 1992, 58(Suppl. 1): Abst O-210.	AU 8942368
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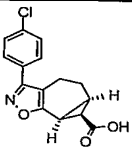
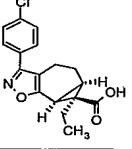
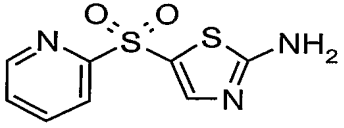
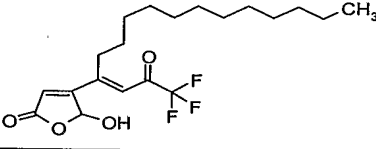
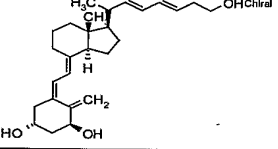
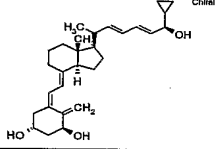
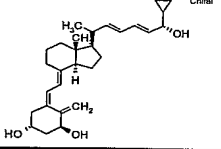
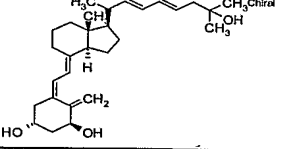
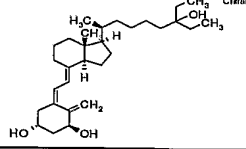
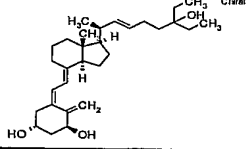
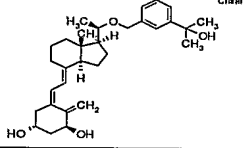
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363	 Chiral	Leo	Binderup, L. et al. Biochem Pharmacol 1991, 42(8): 1569.	EP 460032
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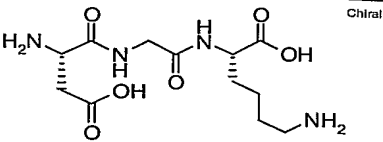
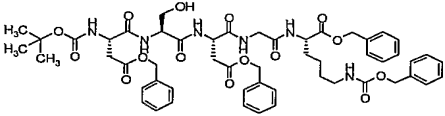
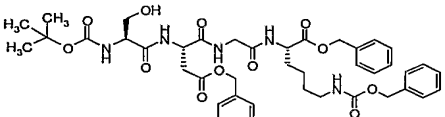
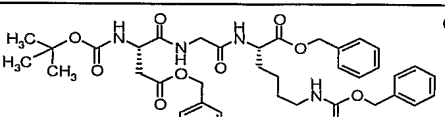
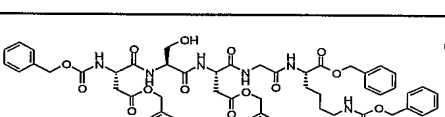
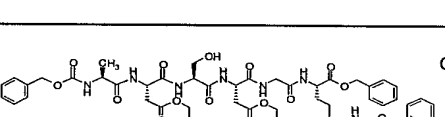
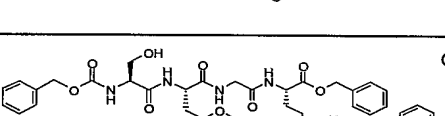
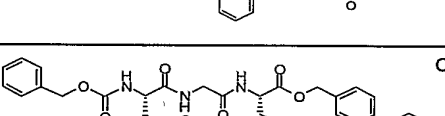
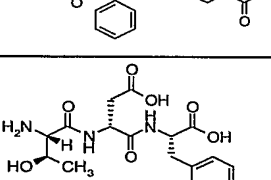
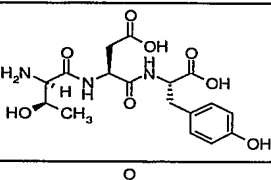
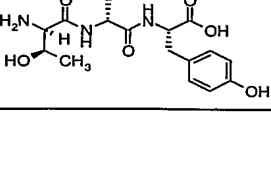
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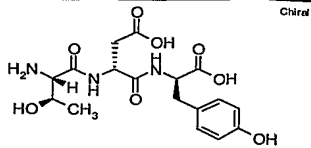
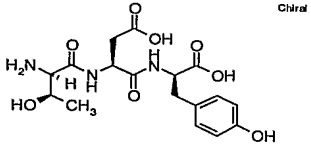
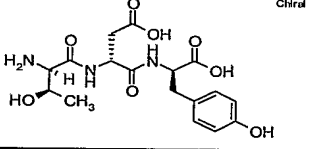
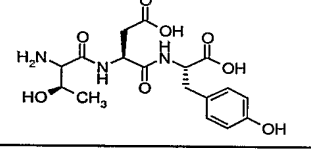
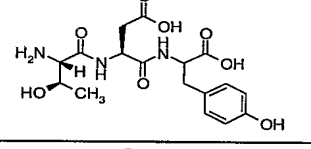
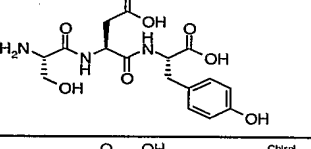
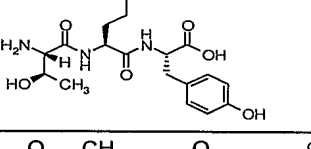
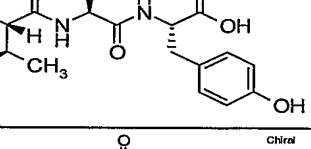
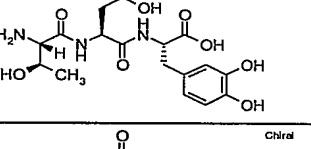
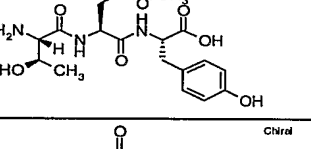
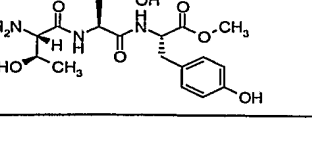
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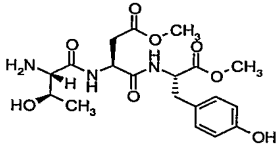
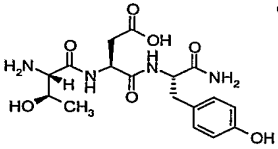
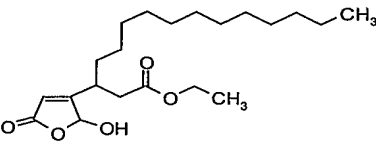
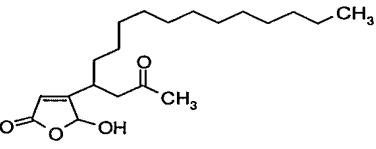
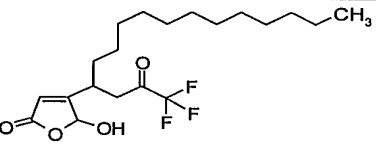
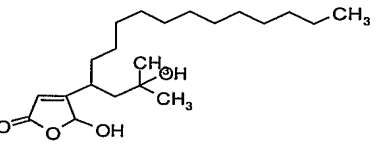
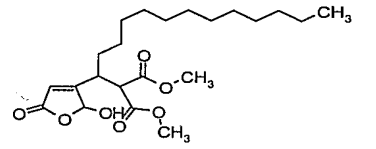
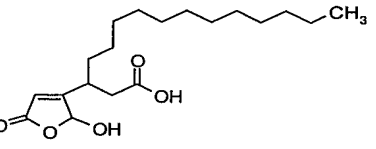
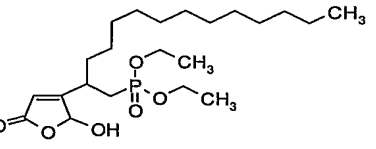
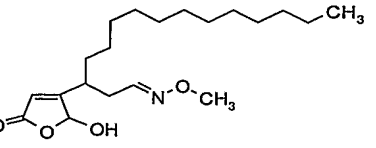
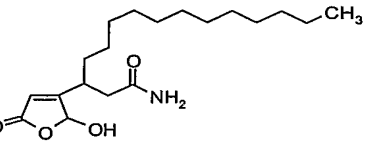
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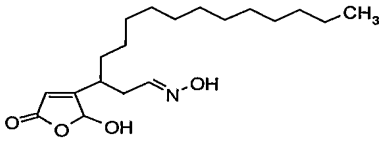
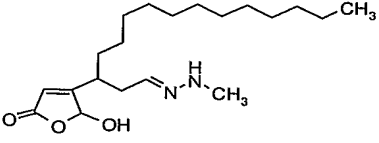
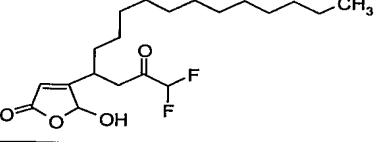
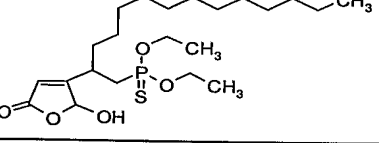
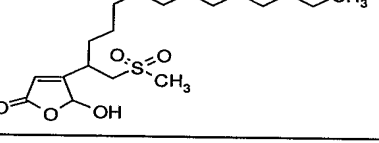
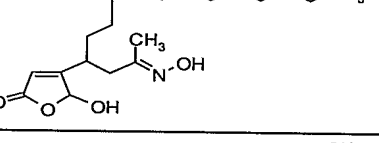
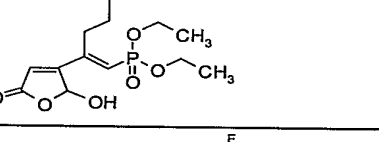
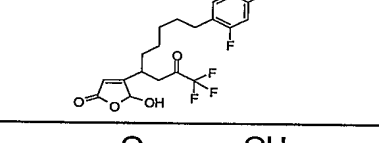
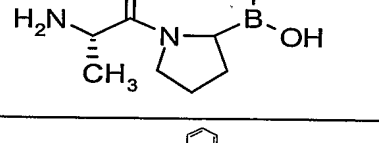
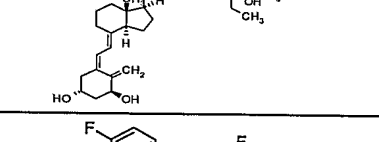
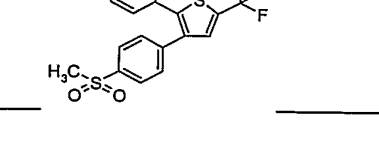
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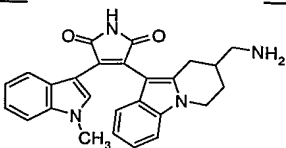
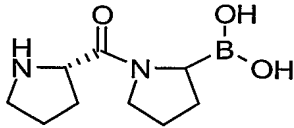
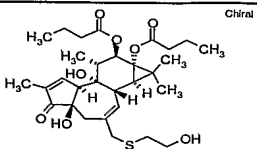
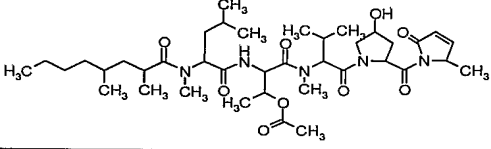
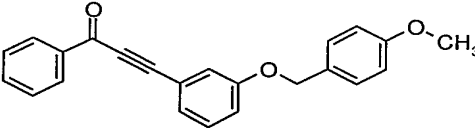
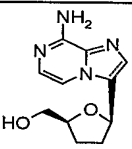
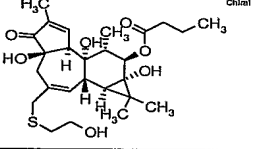
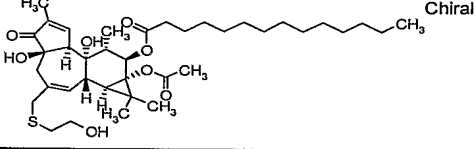
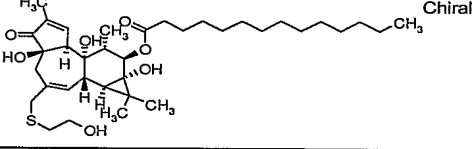
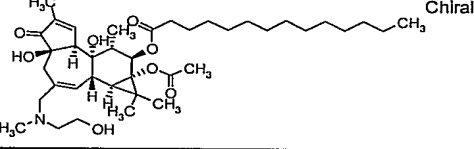
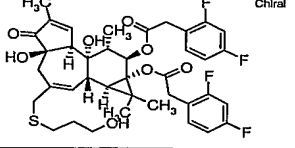
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412		Allergan		US 5013850
413		Leo		WO 9100855
414		Leo		WO 9100855
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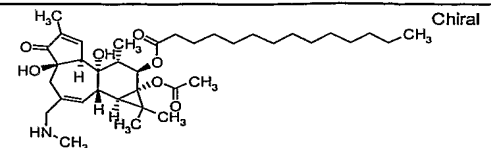
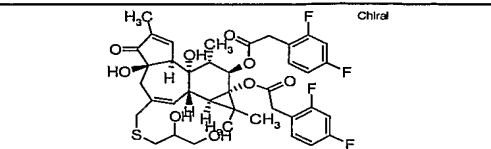
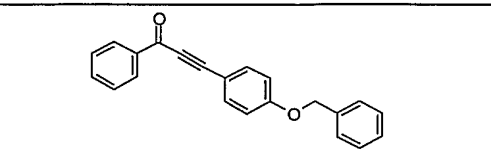
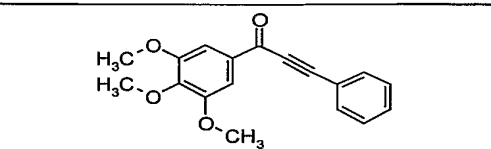
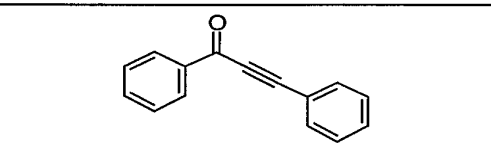
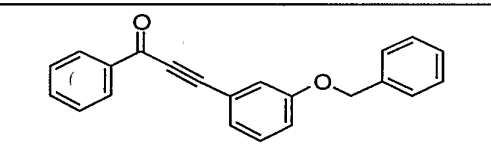
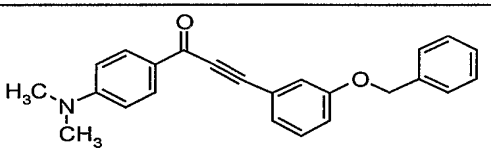
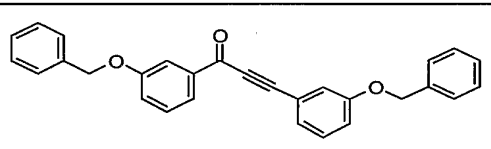
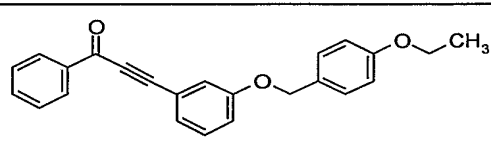
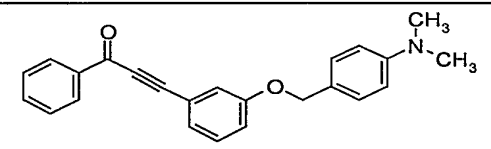
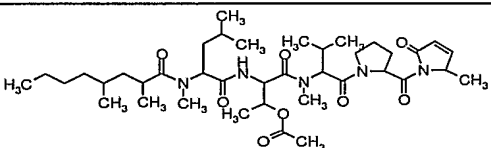
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428	 Chiral	SPA		EP 421074
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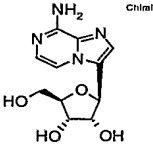
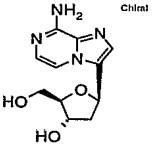
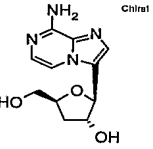
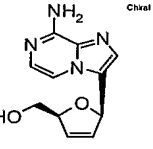
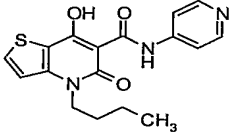
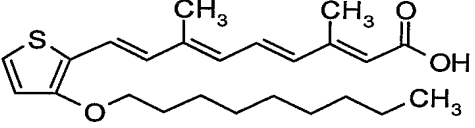
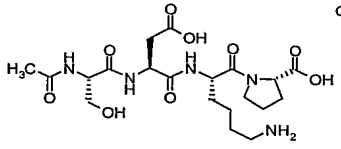
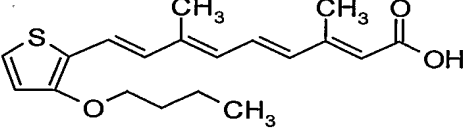
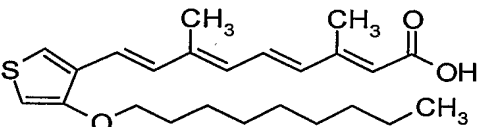
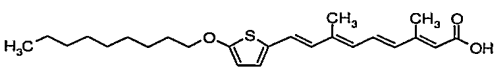
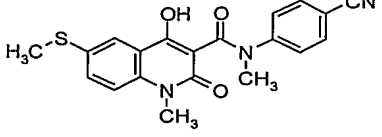
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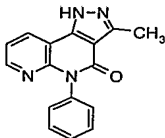
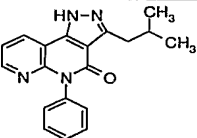
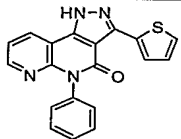
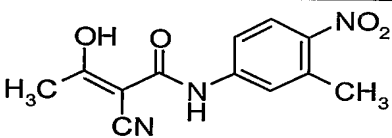
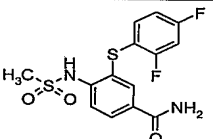
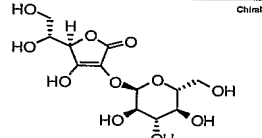
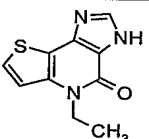
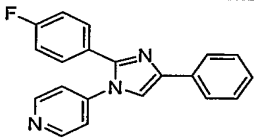
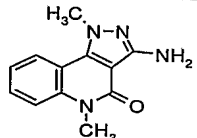
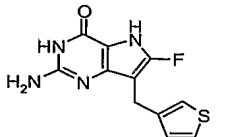
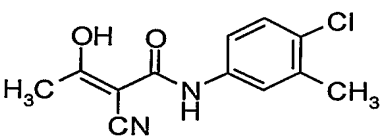
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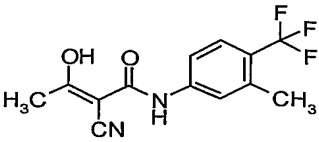
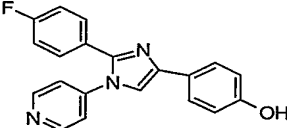
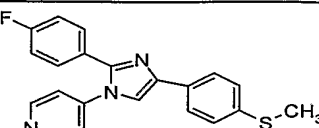
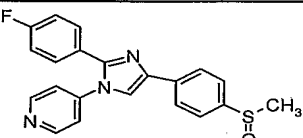
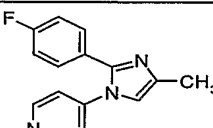
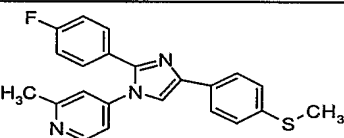
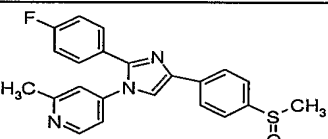
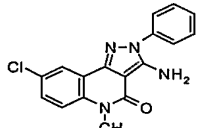
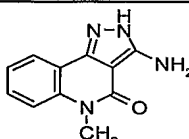

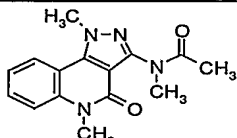
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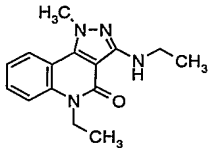
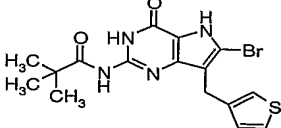
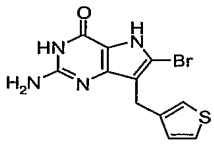
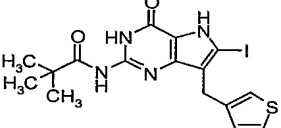
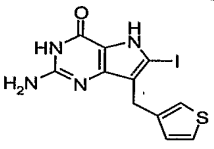
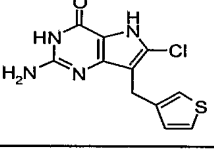
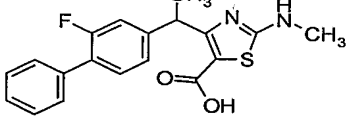
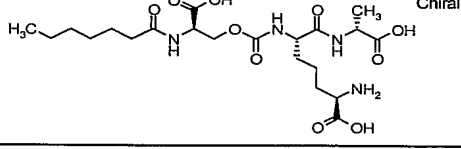
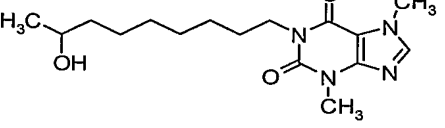
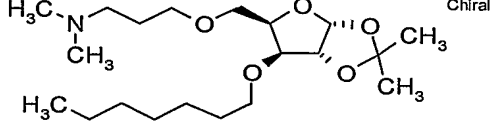

464		Roche	1) Hill, C.H. 6th SCI-RSC Med Chem Symp (Sept 8-11, Cambridge) 1991, Abst S18 .	EP 384349
465		New England Med. Center Hosp.		WO 9116339
466		Alder		US 5145842
467		Harbor Branch Found.		US 5091368
468		Aventis Pharma		EP 476658
469		Merck & Co.		EP 480713
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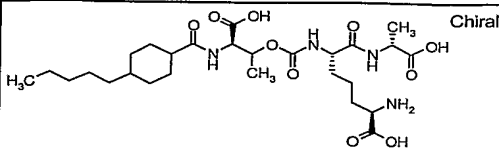
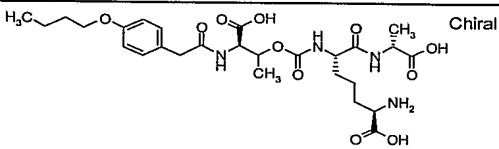
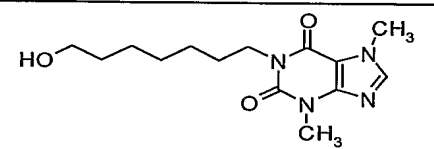
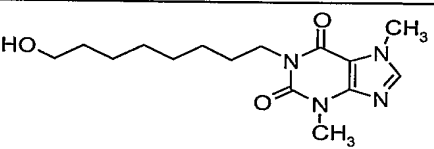
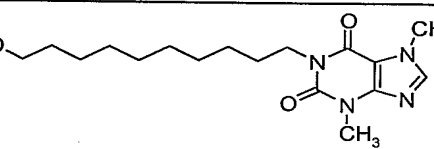
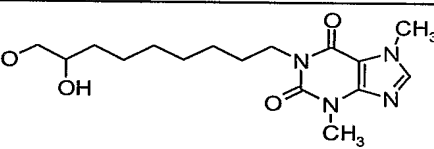
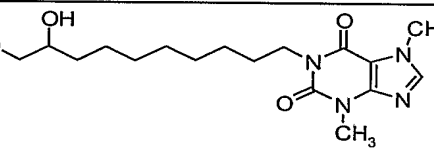
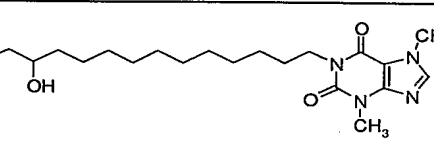
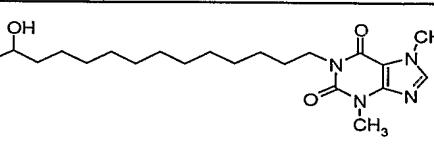
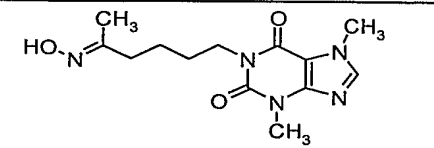
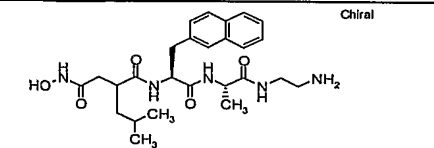
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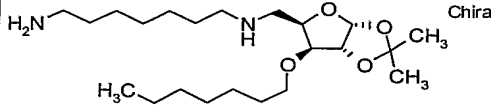
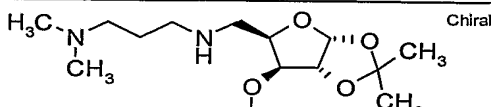
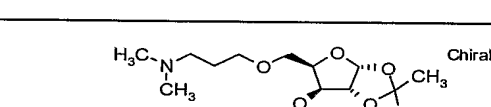
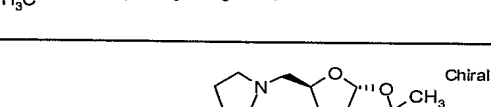
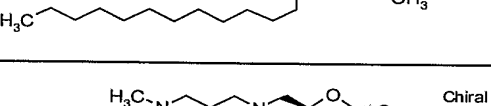
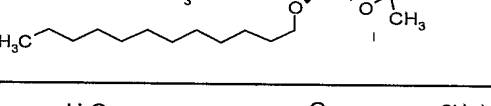
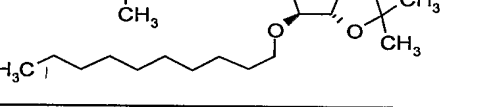
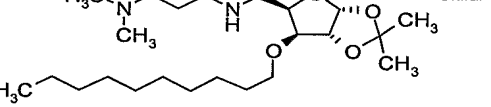
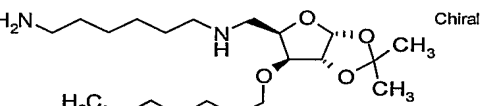
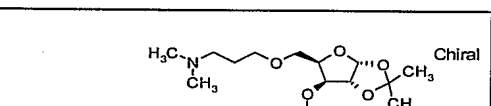
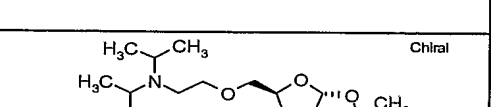
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490		Kyowa Hakko	Miwa, K. et al. 113th Annu Meet Pharmaceut Soc Jpn (March 29-31, Osaka) 1993, Abst 30CC 13-1.	EP 505058
491		Roche		EP 510473
492	 Chiral	Beaufour-Ipsen	1) Carde, P. et al. Proc Amer Soc Clin Oncol 1991, 10: Abst 324.	AU 8810261
493		Roche		EP 510473
494		Roche		EP 510473
495		Roche		EP 510473
496		Fujisawa		WO 9218483

497		Kyowa Hakko		EP 526840
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500		Aventis Pharma		EP 538783
501		Fujisawa	Nakamura, K. et al. Chem Pharm Bull 1993, 41(5): 894.	AU 8783152
502		Hayashibara	1) Yamamoto, I. et al. 18th Int Cong Chemother (June 27- July 2, Stockholm) 1993, Abst 516 .	EP 539196
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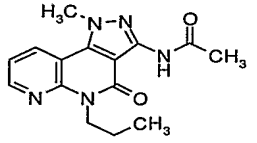
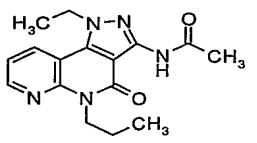
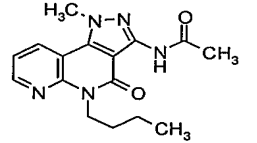
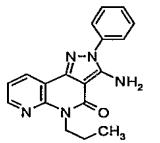
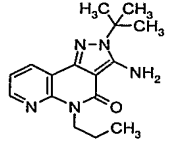
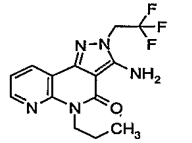
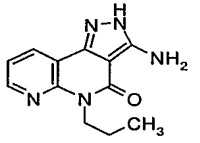
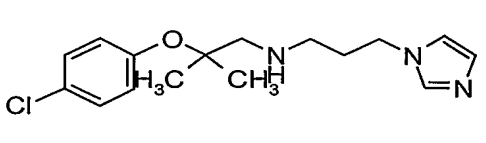
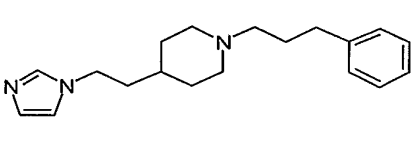
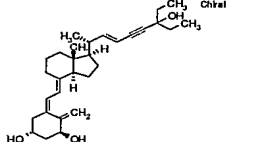
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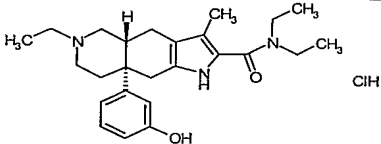
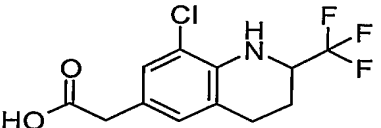
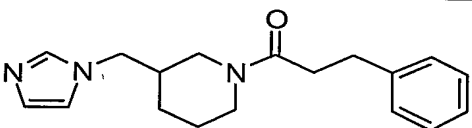
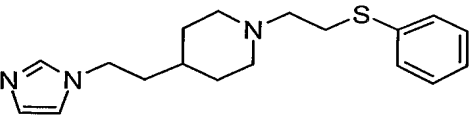
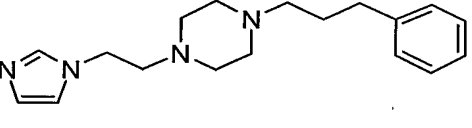
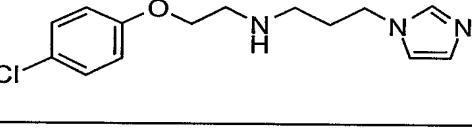
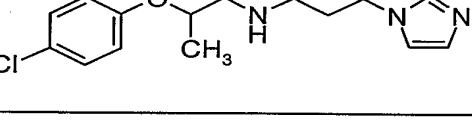
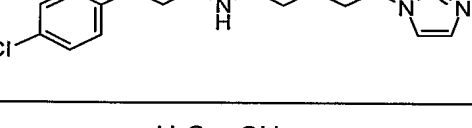
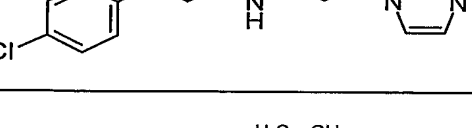
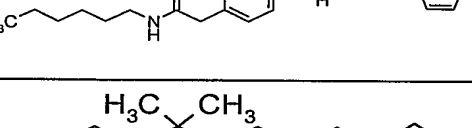
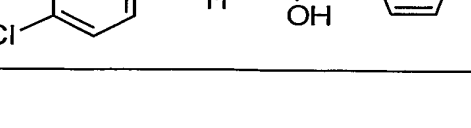
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525		Sumitomo	US 5258396
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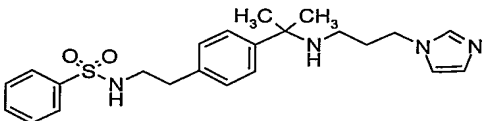
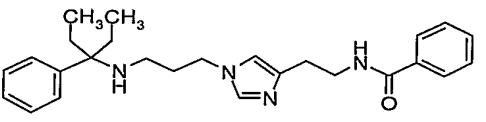
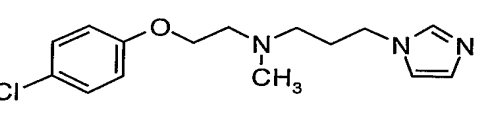
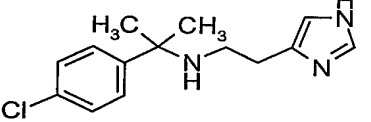
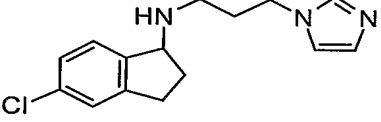
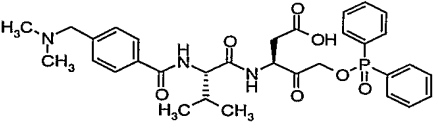
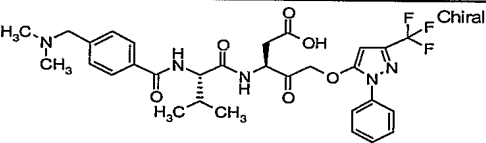
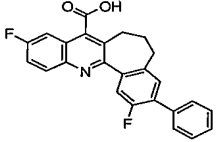
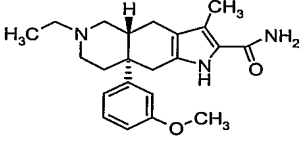
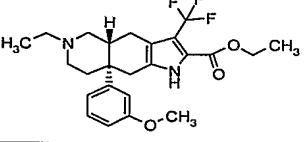
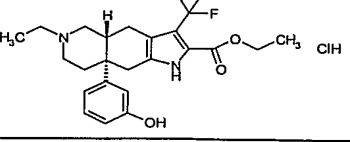
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540	 Chiral	Immunex	1) Immunex Corporation Press Release 1994, July 21. WO 9506031

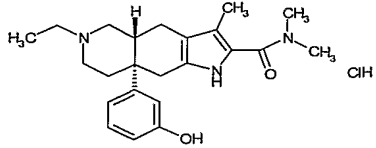
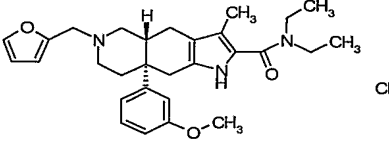
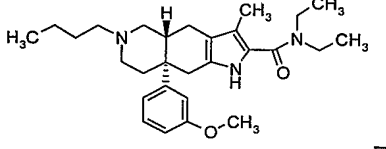
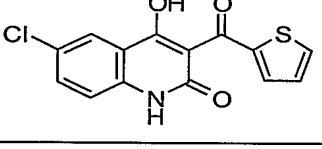
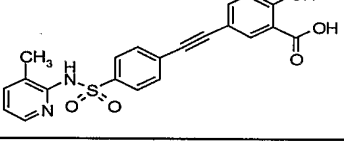
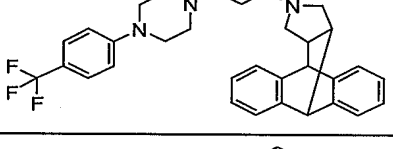
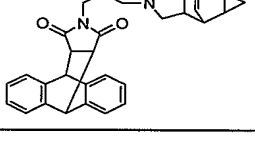
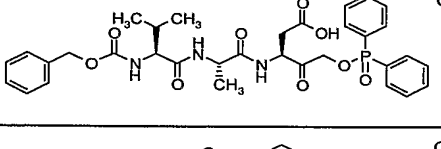
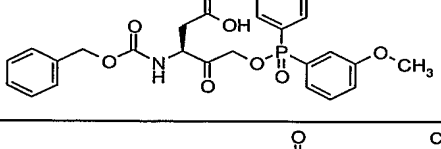
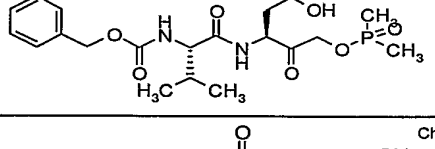
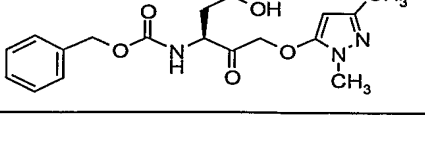
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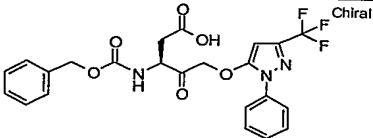
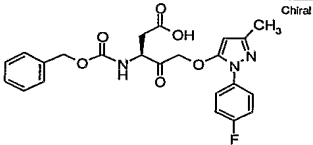
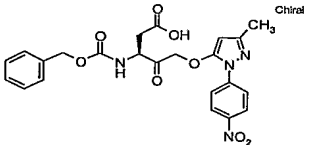
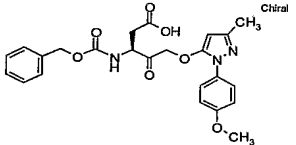
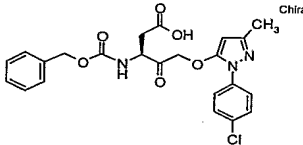
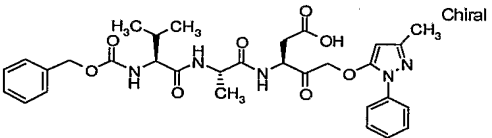
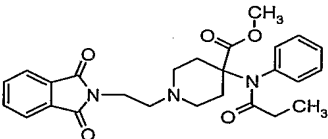
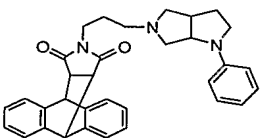
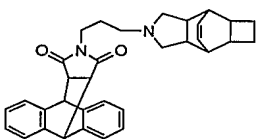
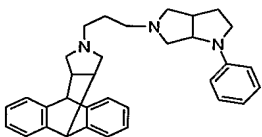
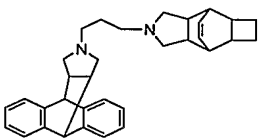
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553	 <chem>c1ccc(cc1)-n2nc3ccccc3n2-c4ccccc4</chem>	British Technol.		GB 2278842
554	 <chem>COC(=O)C(C)=NCCCCCCCCN1C(=O)N(C)C(=O)N1C</chem>	Cell Therapeutics		WO 9416704
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561	 <chem>CC1=C(C2=CC=CC=C2N1C(=O)C3=CC=CC=C3N2)C4=CC=CC=C4N</chem>	Otsuka		JP 94100561
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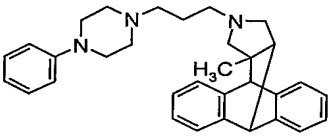
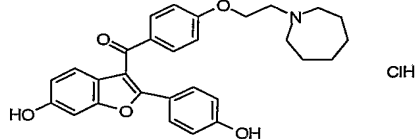
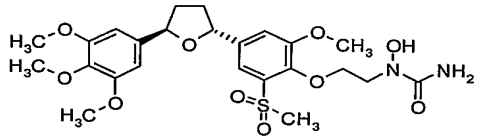
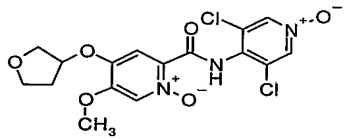
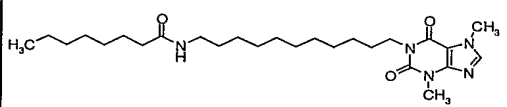
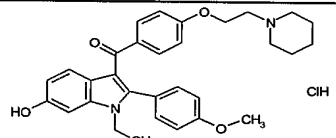
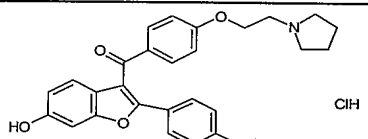
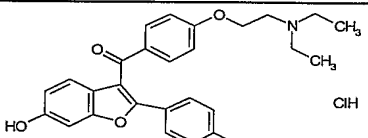
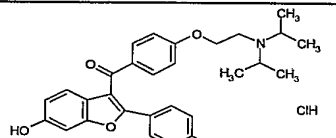
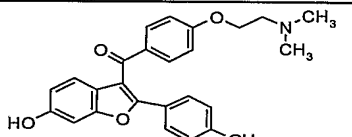
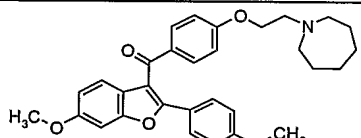
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572	 ClH ClH	Abbott GmbH		WO 9500507
573		Leo		WO 9502577

574		GlaxoSmithKline		WO 9504734
575		Kyorin	Kono, Y. et al. 115th Annu Meet Pharmaceut Soc Jpn (March 29-31, Sendai) 1995, Abst 30 (A3) 10-3.	EP 538477
576		Abbott GmbH		WO 9500507
577		Abbott GmbH		WO 9500507
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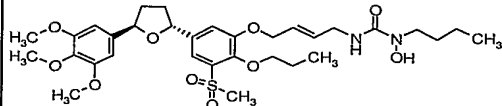
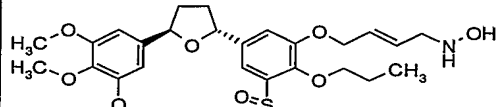
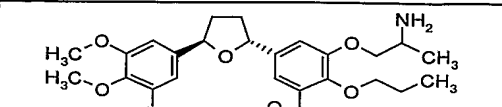
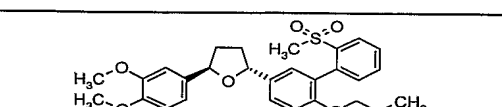
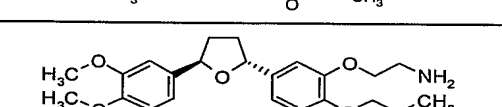
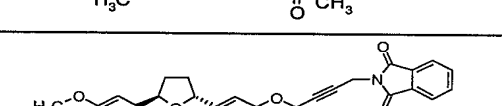
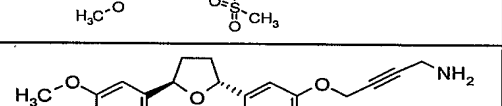
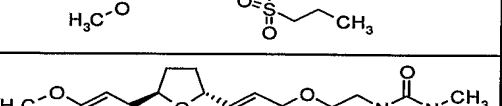
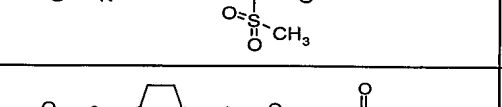
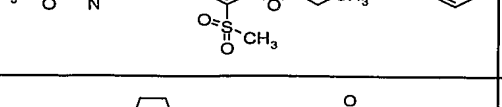
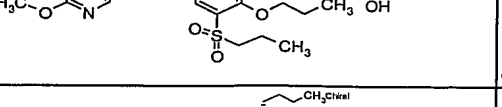
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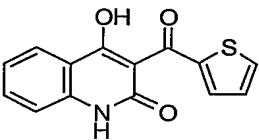
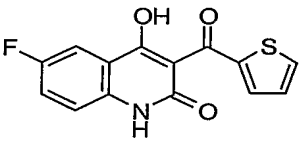
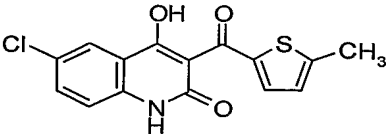
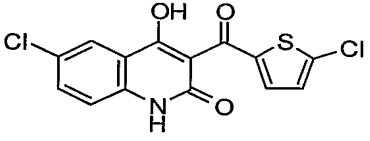
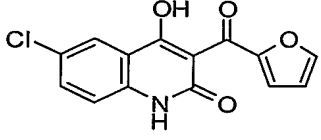
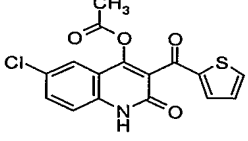
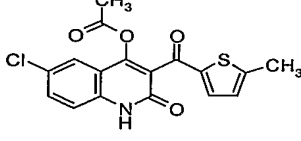
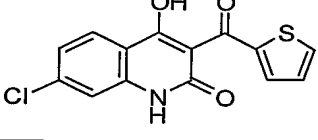
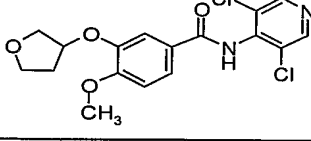
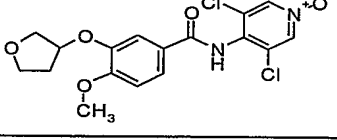
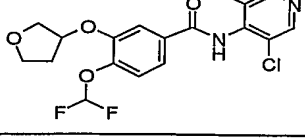
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601		Bayer		US 5409932
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603		Sanofi-Synthelabo	Chiral	EP 644197
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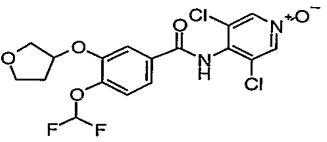
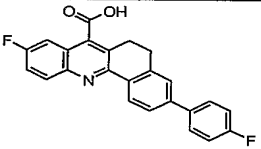
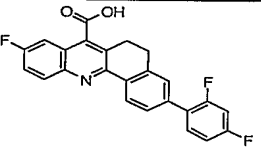
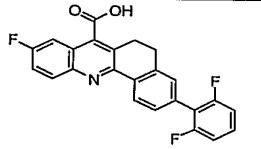
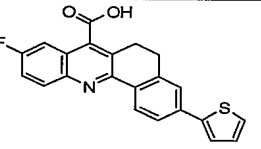
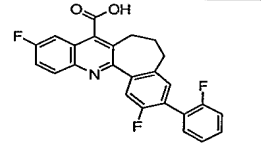
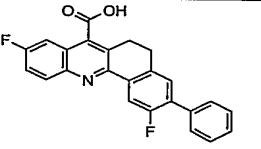
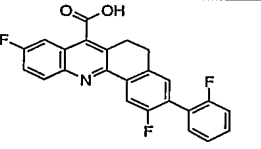
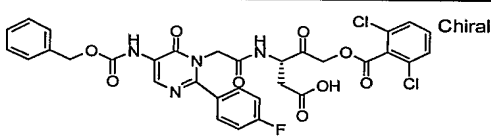
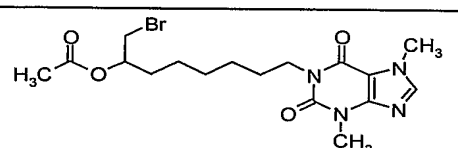
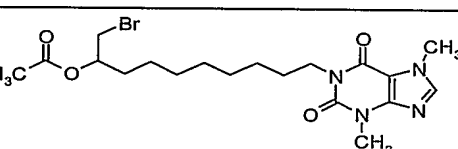
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613		Baxter	France, C.P. et al. Drug Develop Res 1995, 35: 49.	EP 396282
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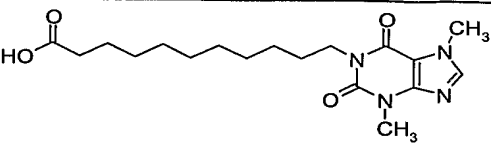
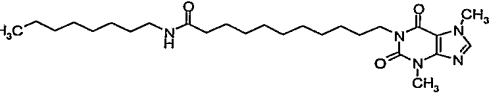
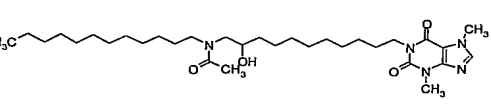
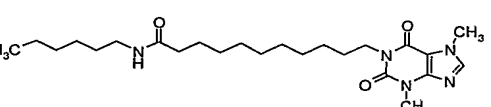
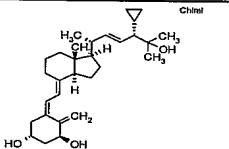
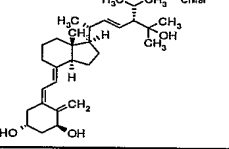
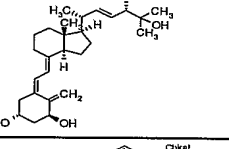
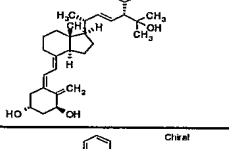
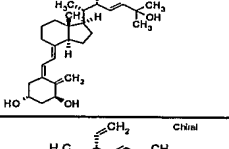
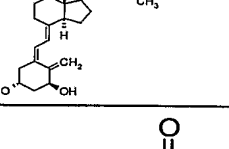
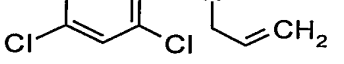
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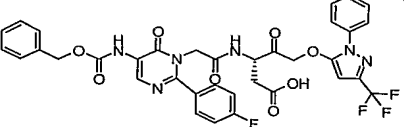
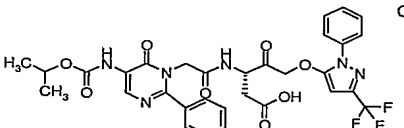
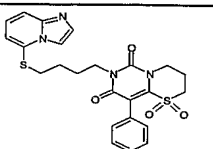
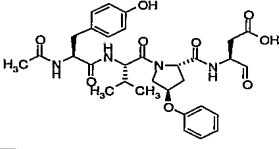
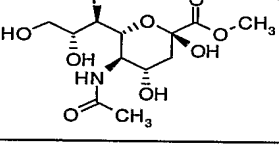
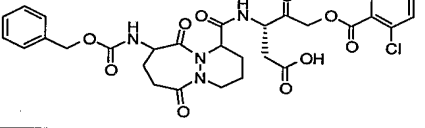
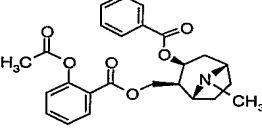
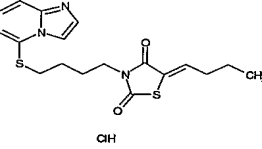
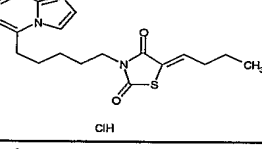
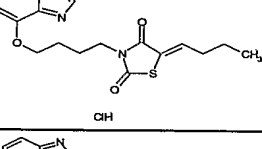
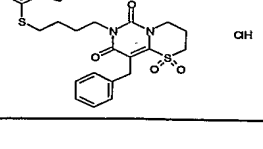
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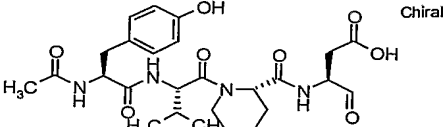
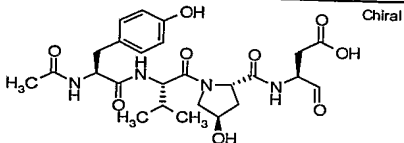
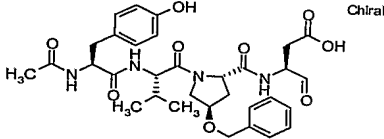
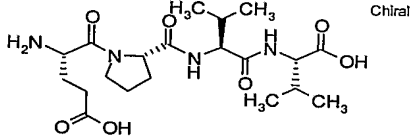
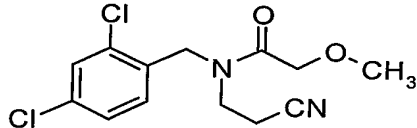

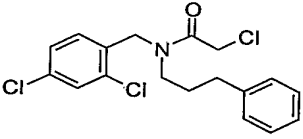
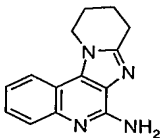
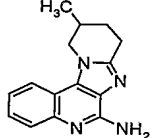
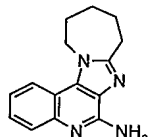
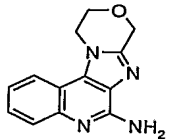
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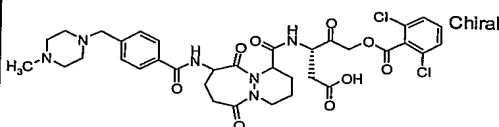
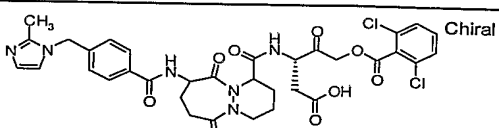
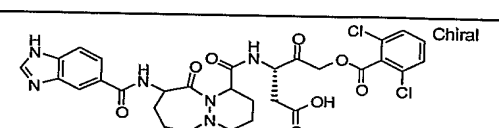
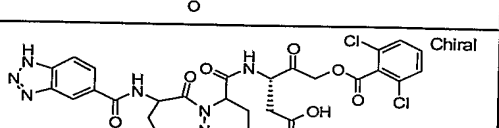
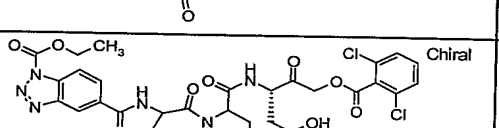
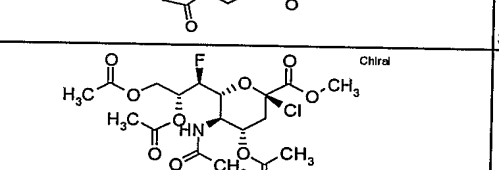
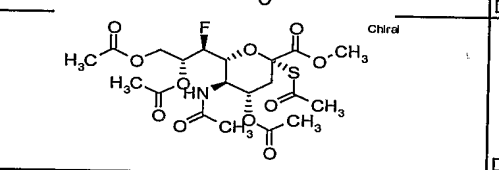
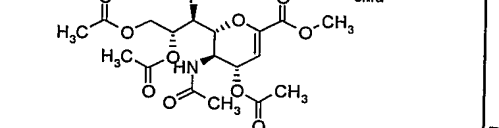
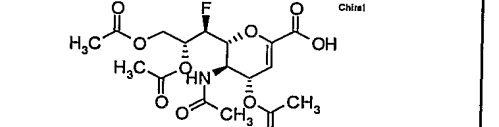
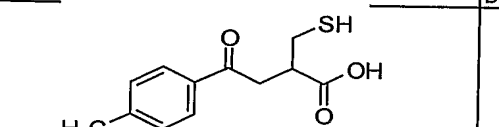
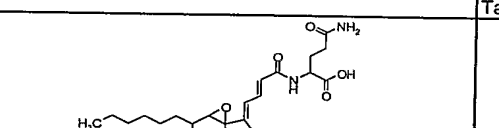
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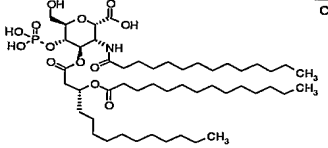
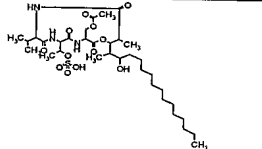
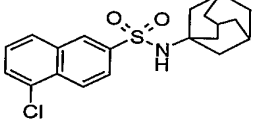
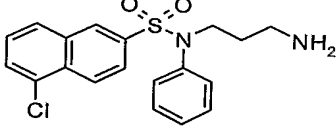
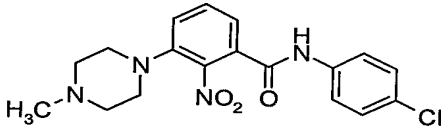
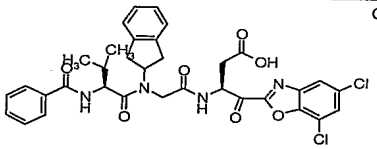
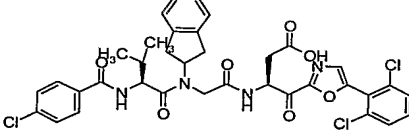
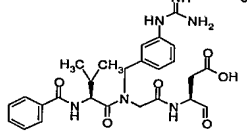
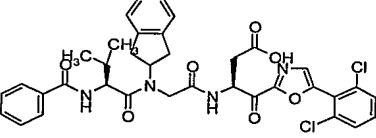
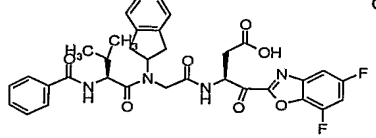
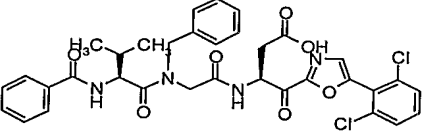
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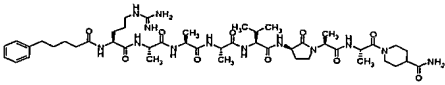
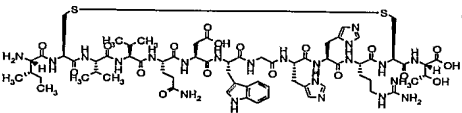
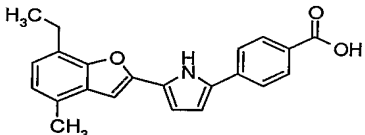
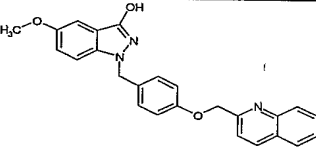
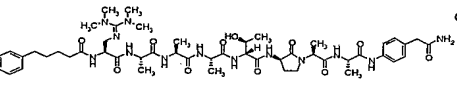
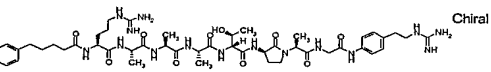
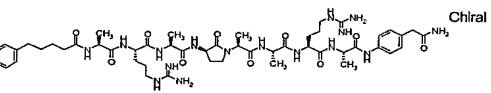
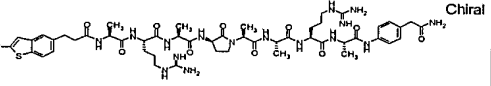
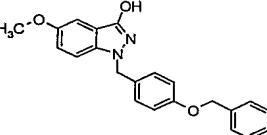
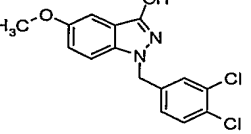
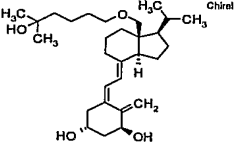
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689	 Chiral	Sanofi-Synthelabo	WO 9533751
690	 OH	Entropin	WO 9534561
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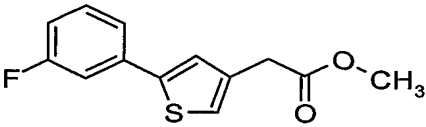
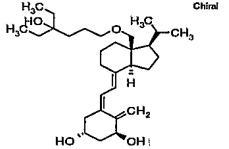
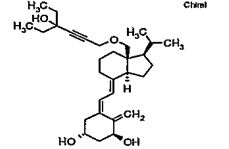
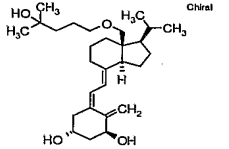
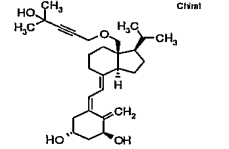
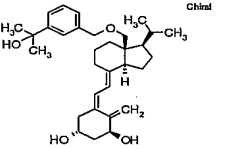
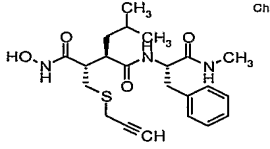
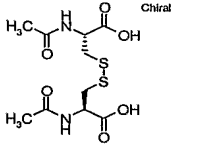
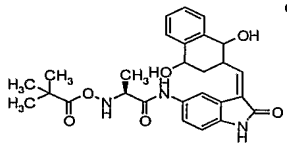
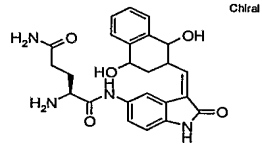
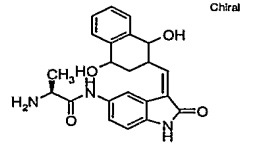
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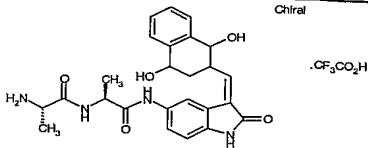
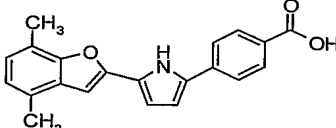
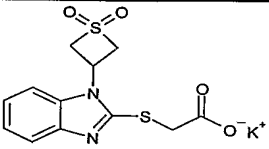
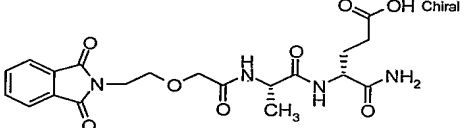
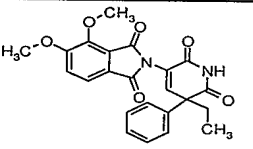
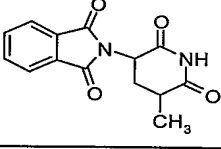
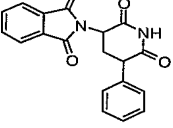
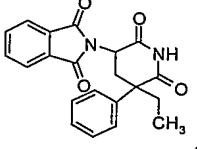
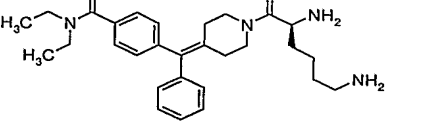
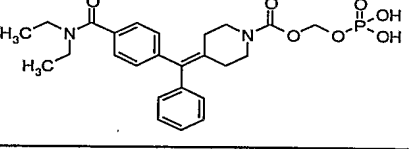
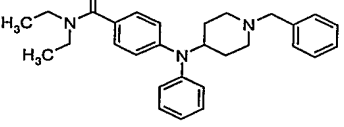
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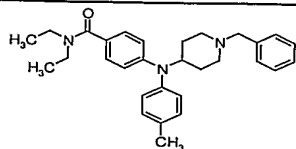
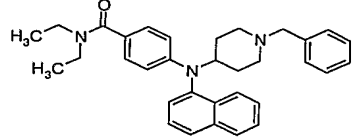
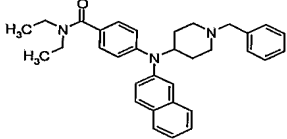
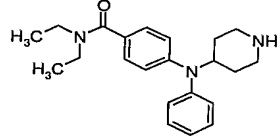
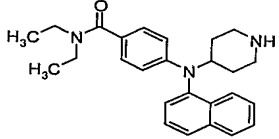
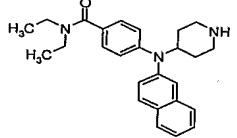
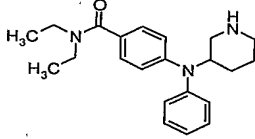
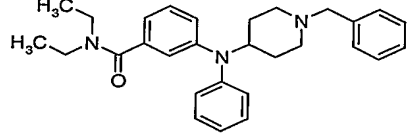
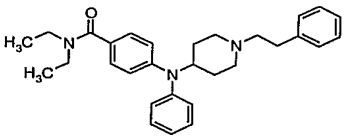
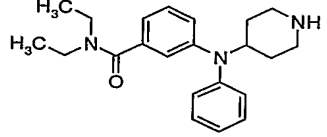
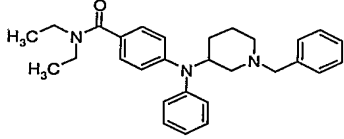
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724	 Chiral	Daikin	EP 711766
725	 Chiral	Daikin	EP 711766
726		Taisho	1) Yoshida, H. et al. Biol Pharm Bull 1997, 20(1): 94. JP 93051358
727		Microbial Chemistry Research Foundation	JP 96176157

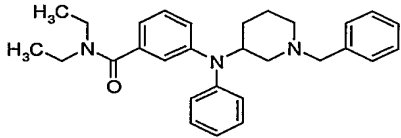
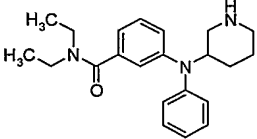
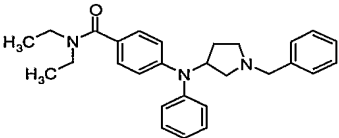
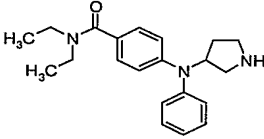
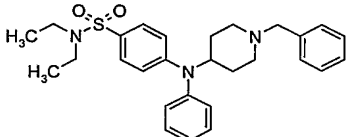
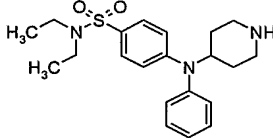
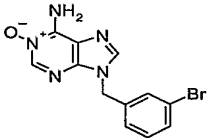
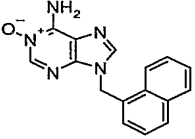
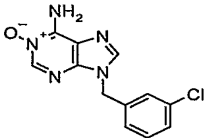
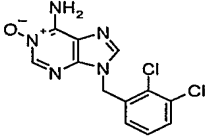
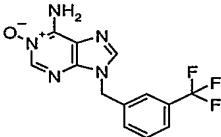
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729	 Chiral	Nippon Kayaku		JP 96283290
730		Tanabe		WO 9640641
731		Tanabe		WO 9640641
732		Daichi Pharmaceutical	1) Kawagoe, K. et al. AFMC Int Med Chem Symp (Sept 3-8, Tokyo) 1995, Abst P13M183.	JP 97059236
733	 Chiral	Vertex		WO 9722618
734	 Chiral	Vertex		WO 9722618
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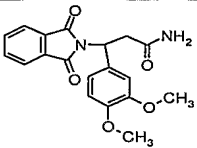
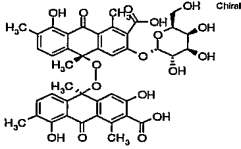
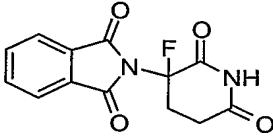
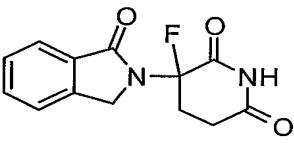
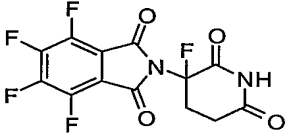
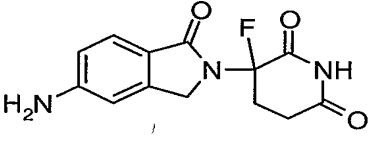
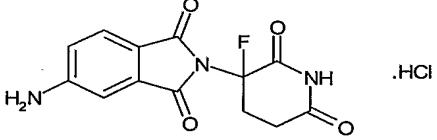
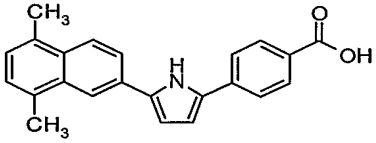
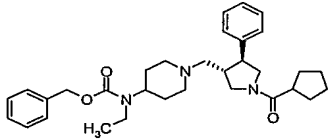
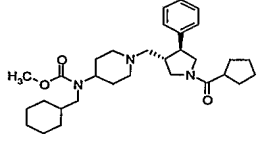
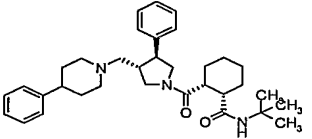
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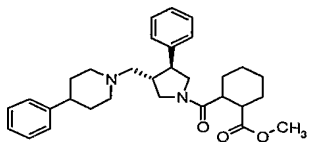
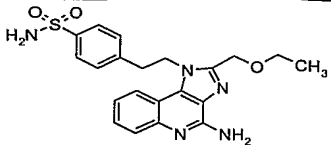
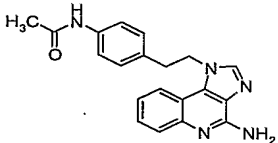
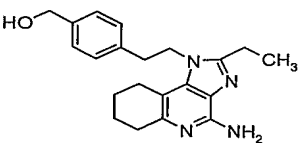
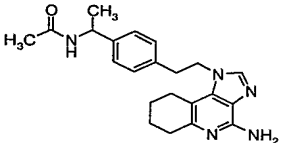
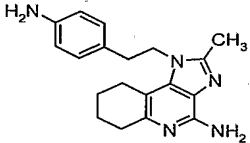
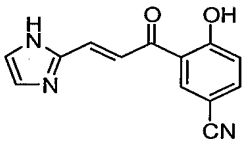
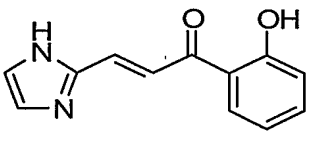
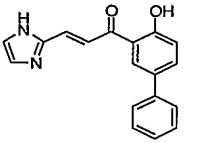
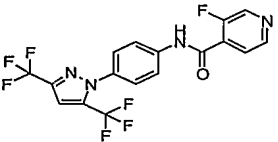
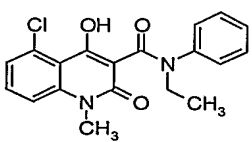
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757		AstraZeneca	1) Saernstrand, B. et al. J Pharmacol Exp Ther 1999, 288(3): 1174.	EP 0463514
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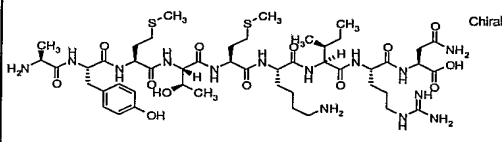
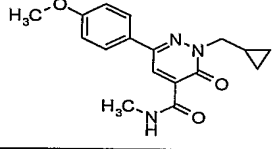
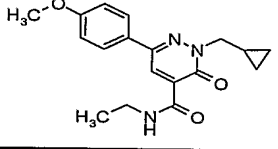
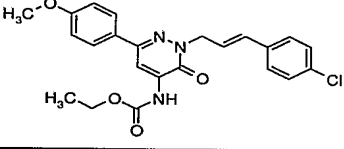
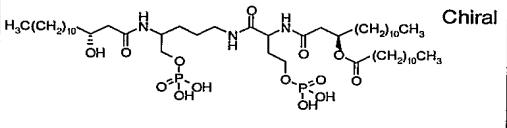
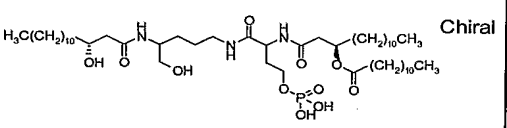
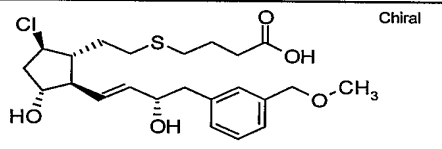
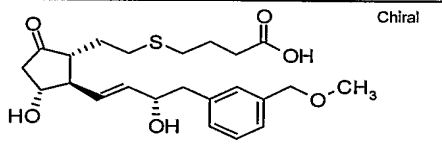
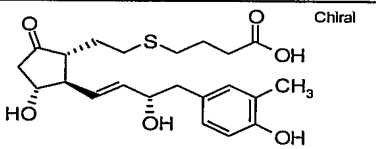
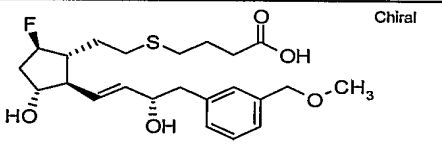
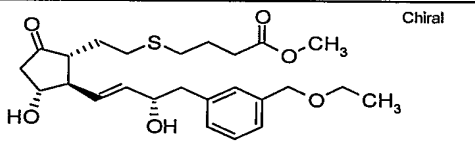
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763		Bashkir Medical University	Sadykov, R.F. et al. Naunyn-Schmied Arch Pharmacol 1998, 358(1, Suppl. 2): Abst P 62.28.	
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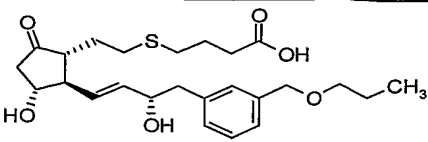
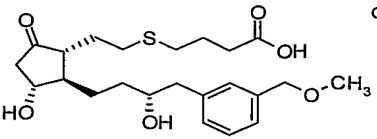
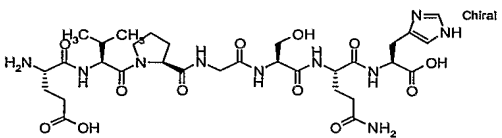
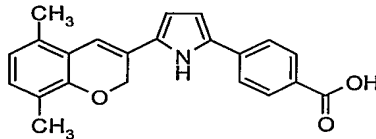
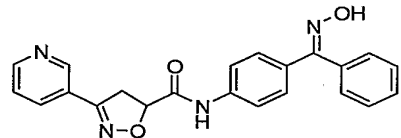
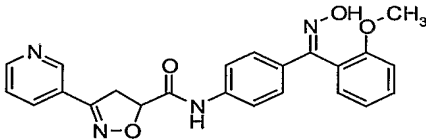
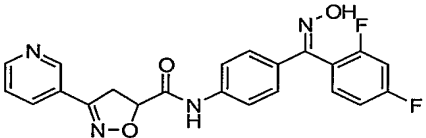
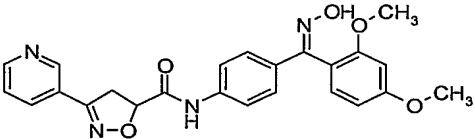
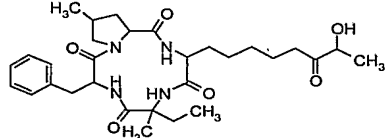
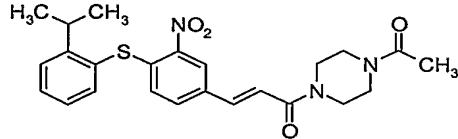
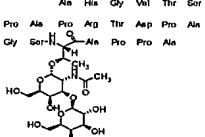
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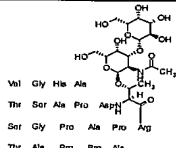
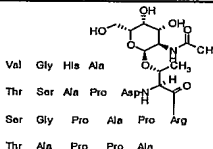
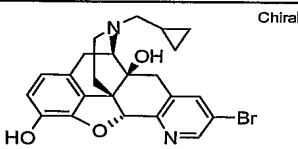
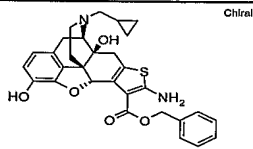
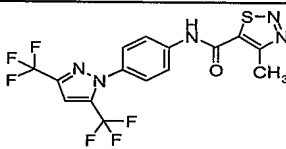
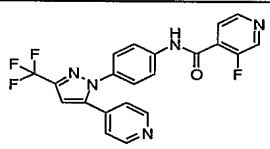
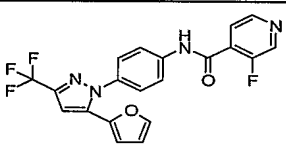
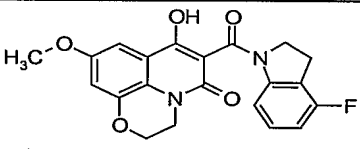
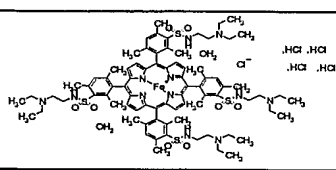
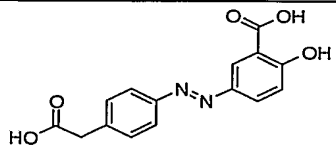
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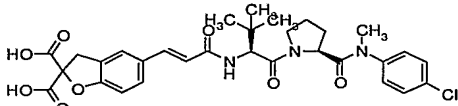
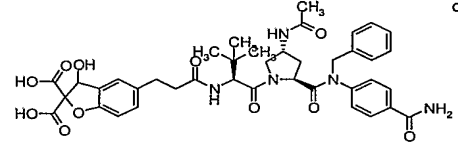
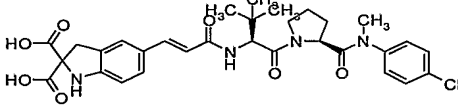
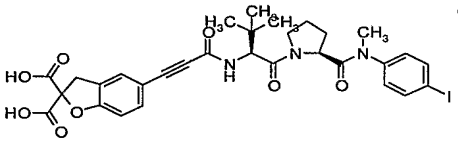
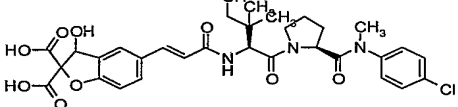
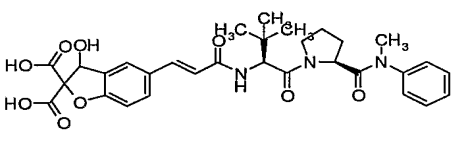
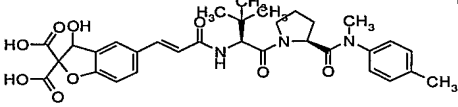
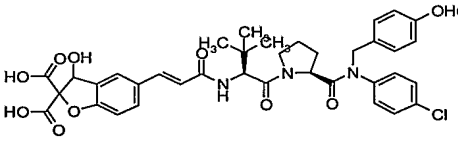
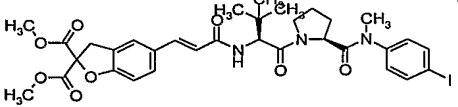
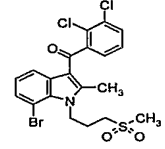
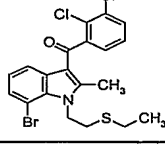
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796		Celgene		US 5874448
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814		Abbott	Madar, D. et al. 222nd ACS Natl Meet (Aug 26-30, Chicago) 2001, Abst MEDI 7.	EP 1068187
815		Active Biotech		WO 9955678

816		Amersham	1) Gesser, B. et al. Proc Natl Acad Sci USA 1997, 94(26): 14620.	WO 9601318
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835		Fujisawa		WO 0021979
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837		Cancer Research UK		WO 0052046

838	 <p>Val Gly His Ala Thr Ser Ala Pro Asp His Arg Thr Ala Pro Pro Ala</p>	Cancer Research UK		WO 0052046
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842		Abbott Labs.		EP 1068187
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845		Fujisawa	Spears, G. et al. 21st Symp Med Chem (Nov 28-30, Kyoto) 2001, Abst 2P-29.	
846	<p>Val His Phe Phe Arg Asn Ile Pro Thr Arg Ala Thr Val</p>	Austin Research Institute	Tselios, T. et al. J Med Chem 2002, 45(2): 275.	
847		Eukarion		WO 0204454
848		Nobex	1) Riggs-Sauthier, J.A. et al. 224th ACS Natl Meet (Aug 18-22, Boston) 2002, Abst MEDI 305.	WO 0218324

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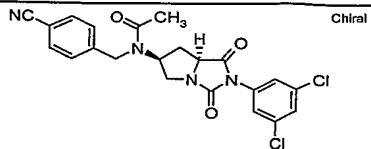
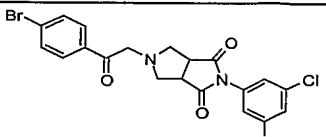
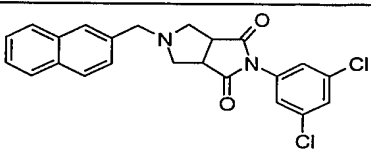
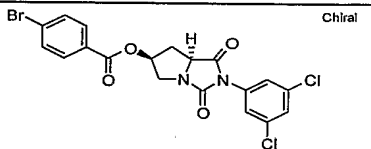
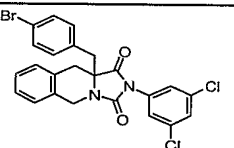
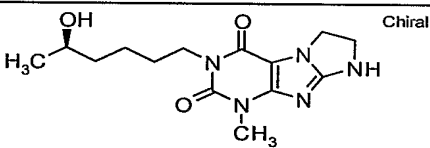
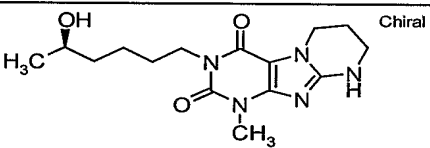
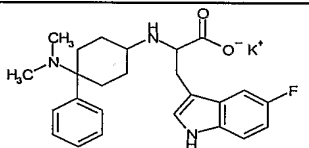
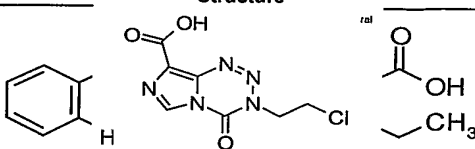
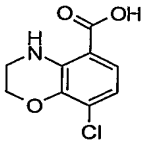
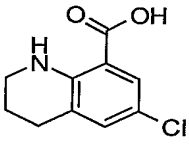
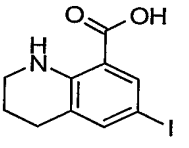
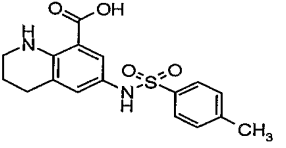
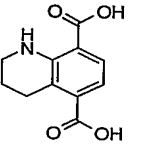
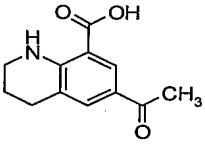
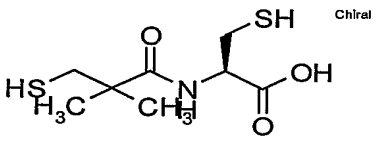
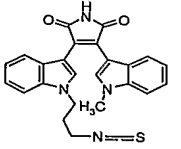
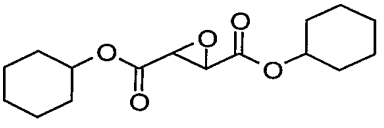
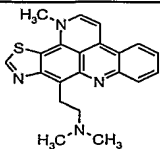
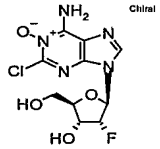
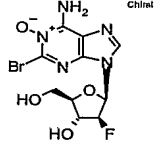
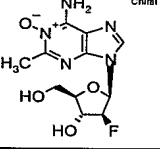
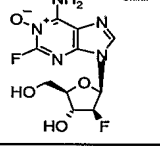
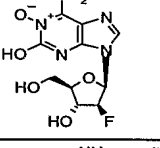
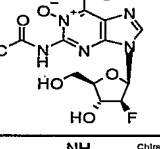
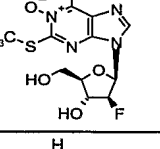
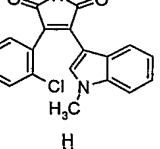
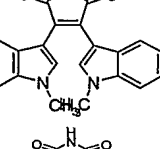
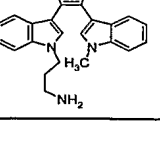
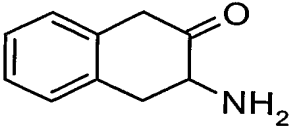
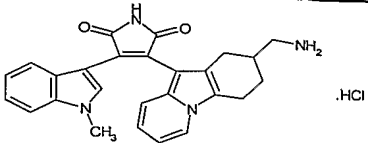
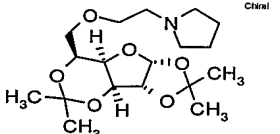
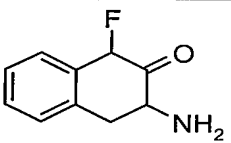
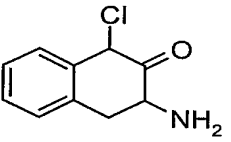
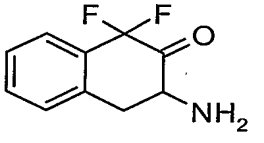
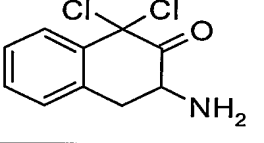
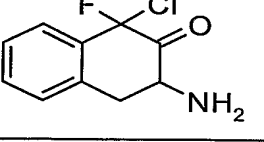
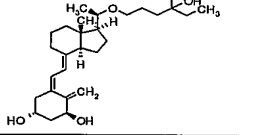
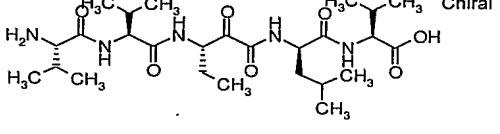
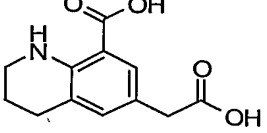
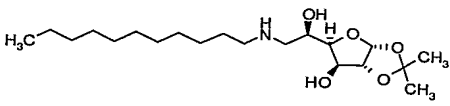
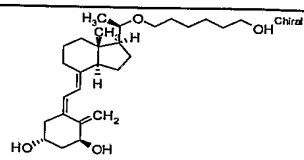
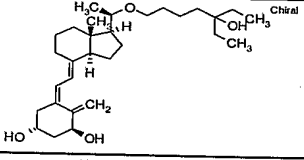
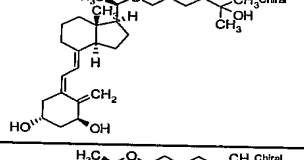
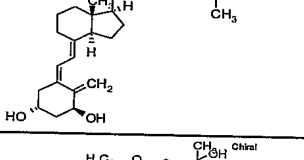
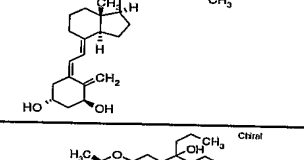
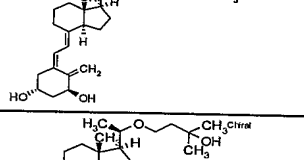
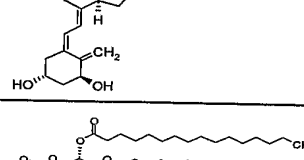
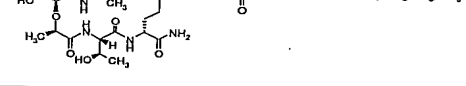
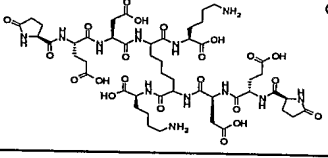
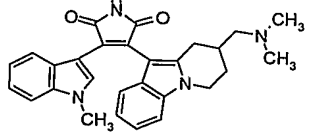
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878		Gruenenthal	WO 0290317

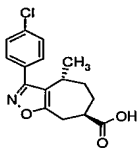
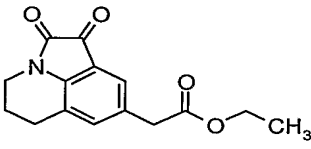
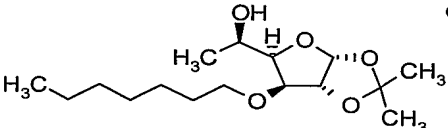
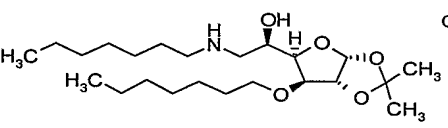
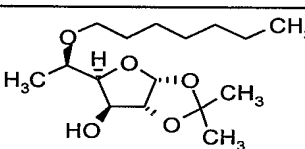
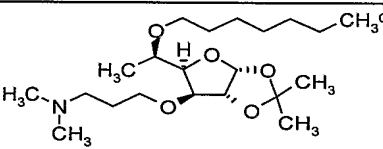
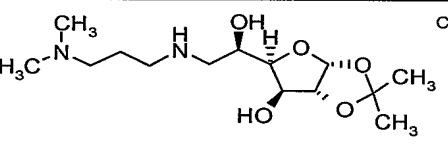
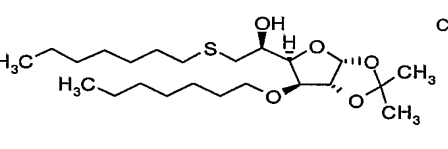
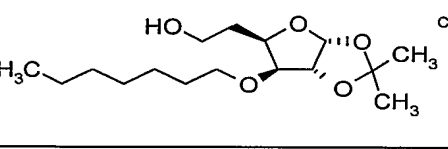
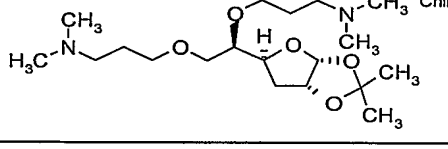
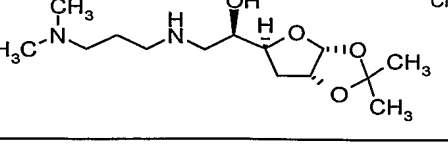
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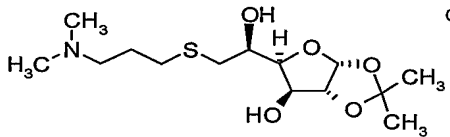
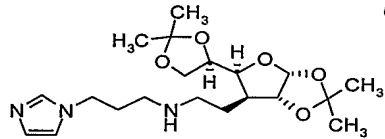
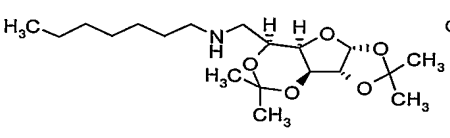
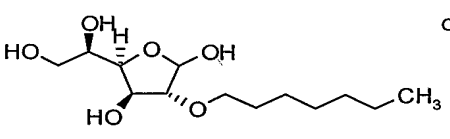
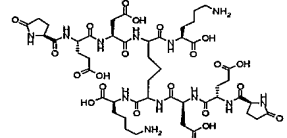
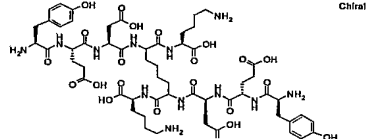
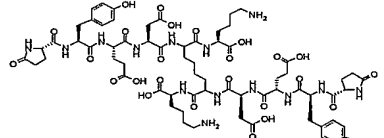
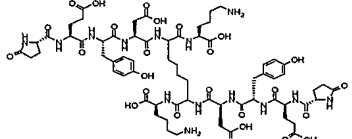
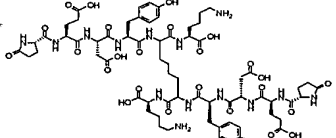
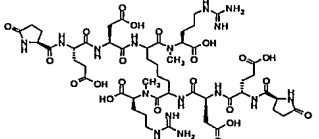
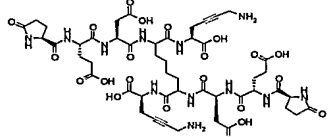
Compound #	Structure	Source	Literature Reference	Patent Number
881		May & Baker		EP 252682
882		Kyorin		EP 310096
883		Kyorin		EP 310096
884		Kyorin		EP 310096
885		Kyorin		EP 310096
886		Kyorin		EP 310096
887		Kyorin		EP 310096
888		Santen		EP 326326
889		Roche		AU 8929658
890		Taisho	1) Takeshita, K. et al. Int J Immunother 1988, 4(2): 97-106.	JP 79141750

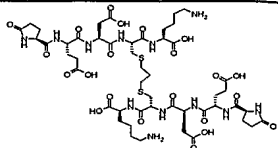
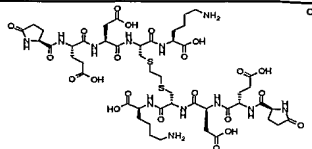
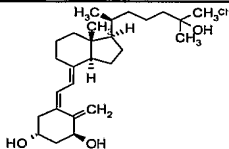
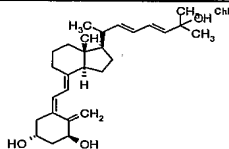
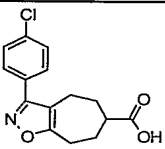
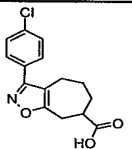
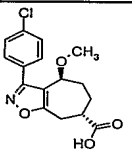
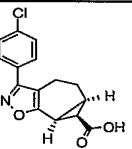
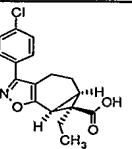
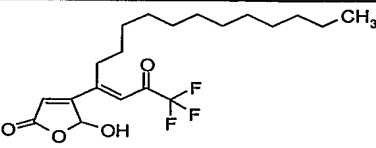
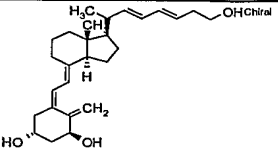
891		Harbor Branch Found.	1) Burres, N.S. et al. Proc Amer Assoc Cancer Res 1989, 30: Abst 1914.	EP 331320
892		Scripps Clinic Res. Found.		WO 8908658
893		Scripps Clinic Res. Found.		WO 8908658
894		Scripps Clinic Res. Found.		WO 8908658
895		Scripps Clinic Res. Found.		WO 8908658
896		Scripps Clinic Res. Found.		WO 8908658
897		Scripps Clinic Res. Found.		WO 8908658
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899		Roche		AU 8929658
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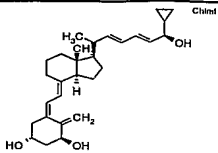
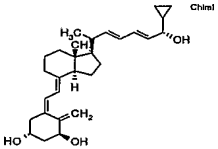
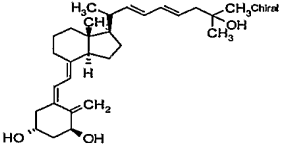
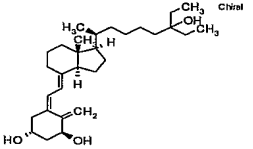
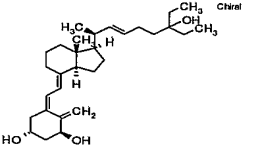
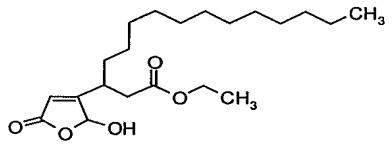
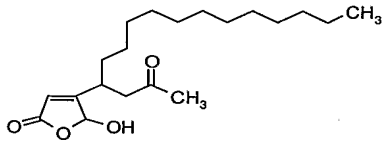
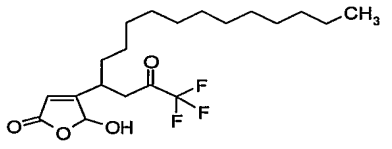
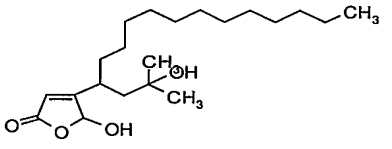
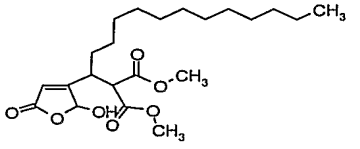
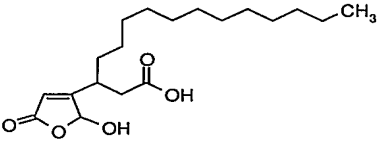
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910		Leo	Binderup, L. et al. Biochem Pharmacol 1991, 42(8): 1569.	EP 460032
911		Microbial Chemistry Research Foundation	Muraoka, Y. et al. 30th Intersci Conf Antimicrob Agents Chemother (Oct 21-24, Atlanta) 1990, Abst 801 .	
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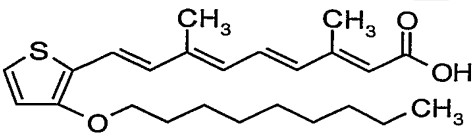
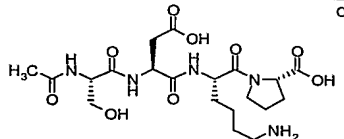
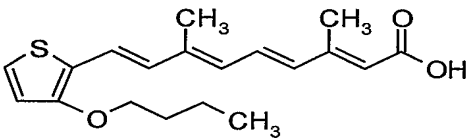
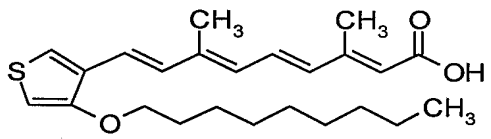
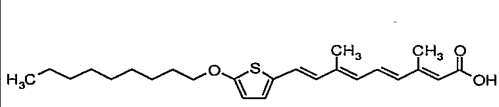
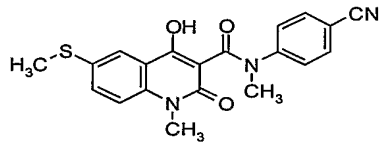
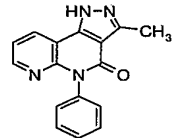
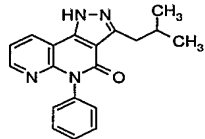
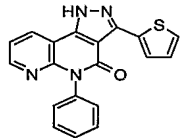
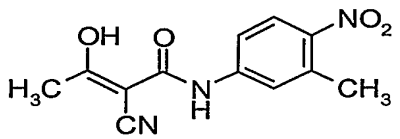
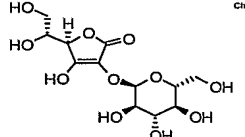
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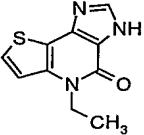
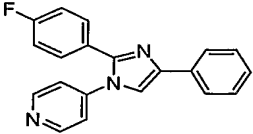

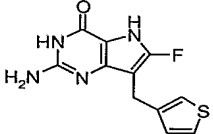
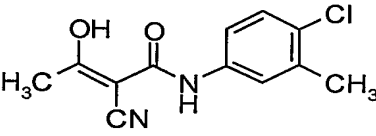
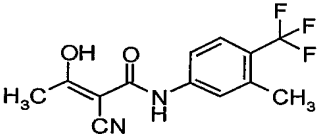
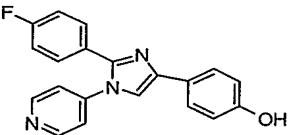
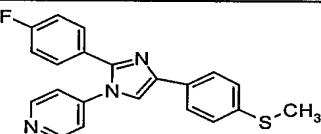
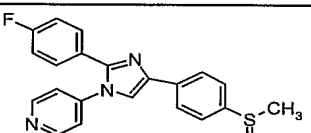
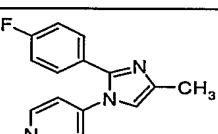
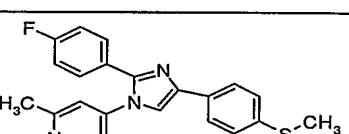
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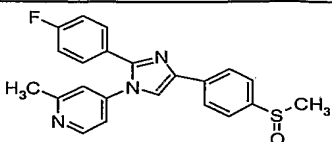
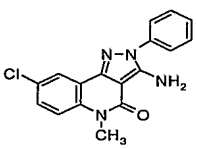
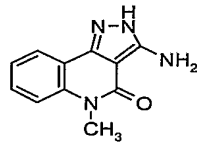

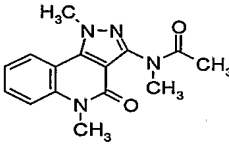
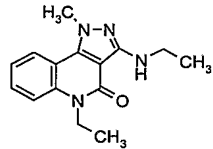
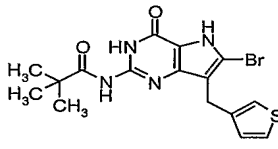
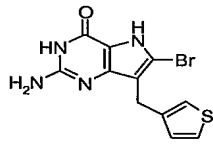
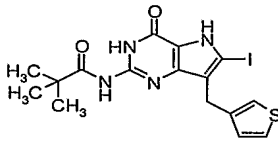
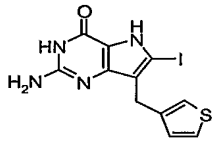
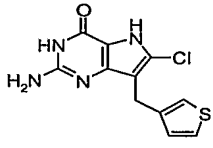
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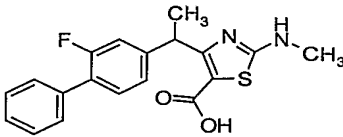
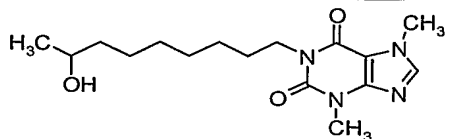
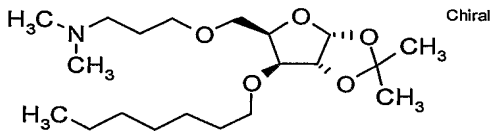
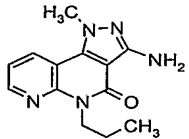
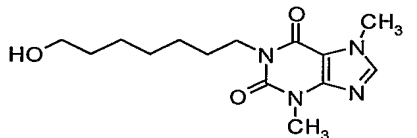
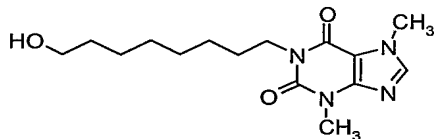
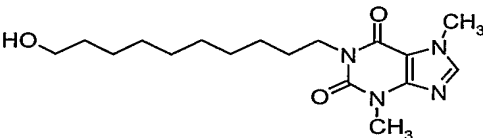
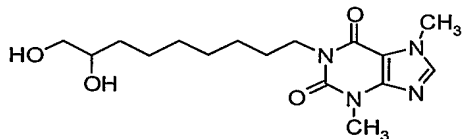
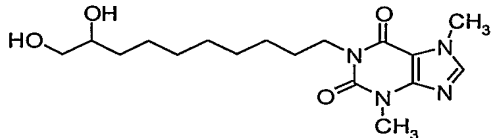
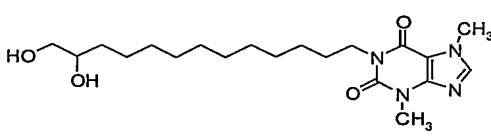
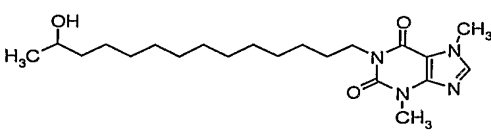
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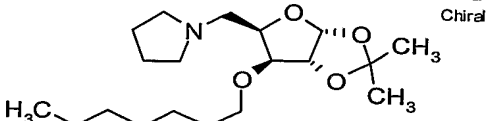
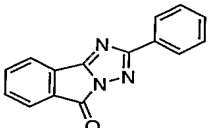
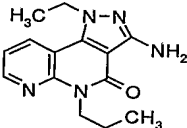
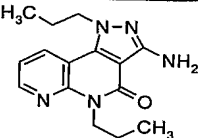
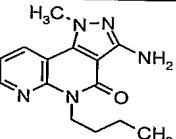
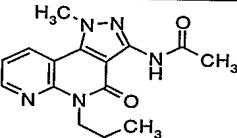
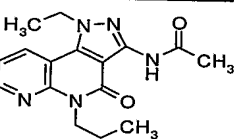
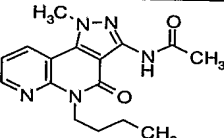
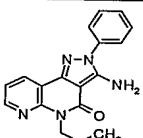

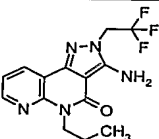
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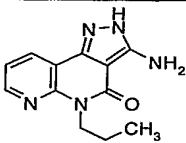
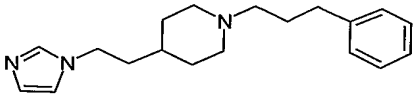
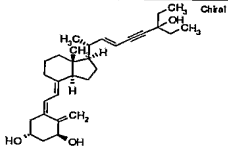
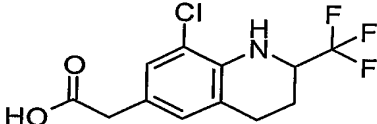
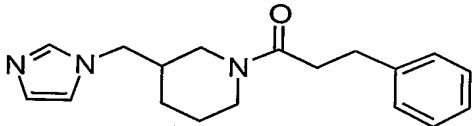
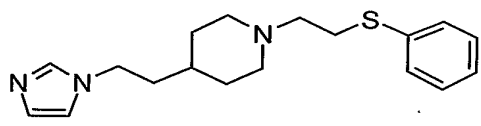
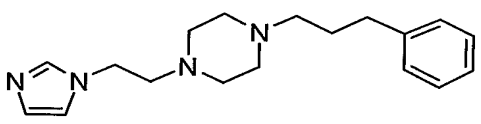
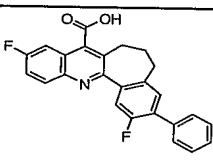
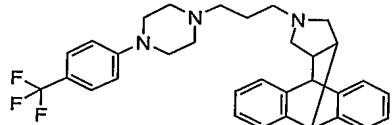
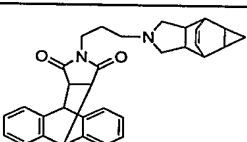
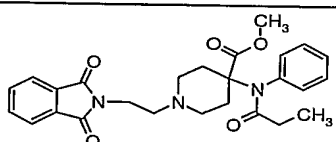
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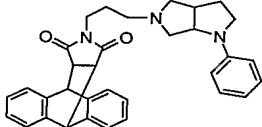
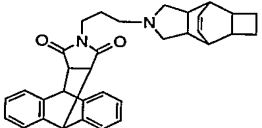
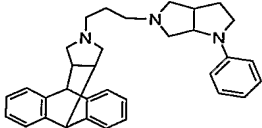
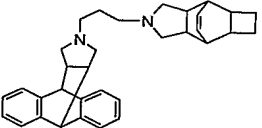
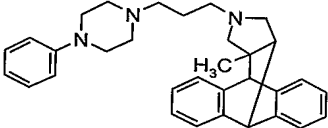
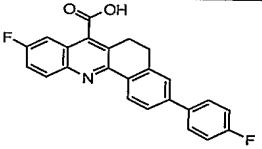
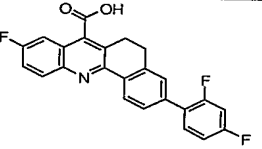
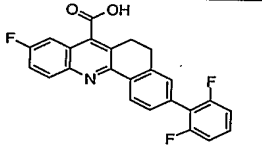
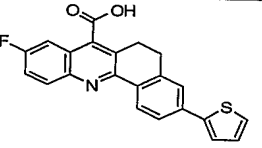
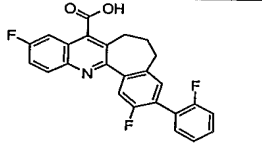
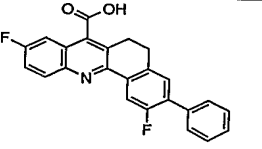
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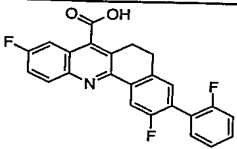
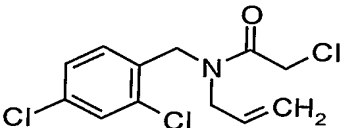
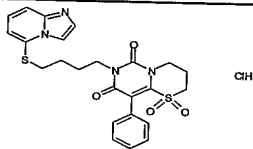
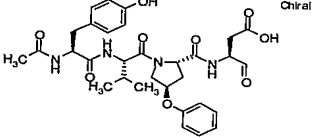
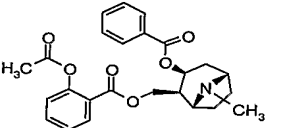
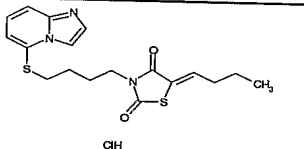
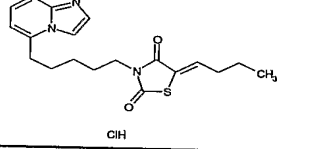
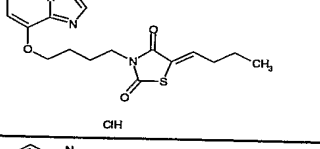
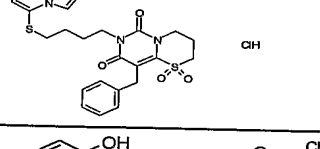
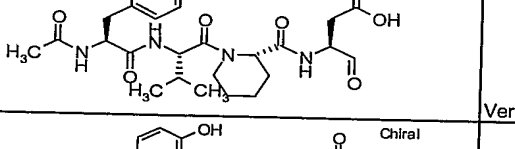
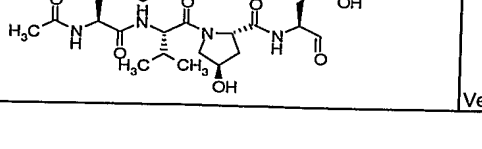
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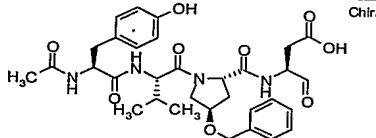
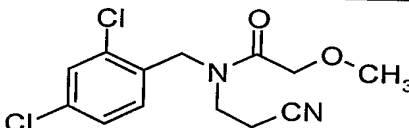
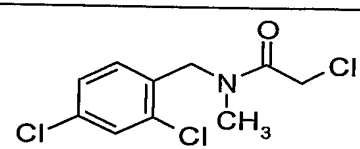
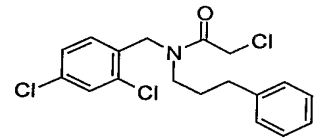
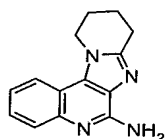
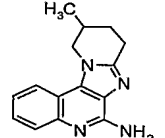
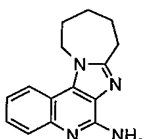
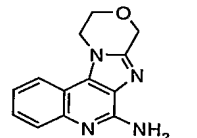
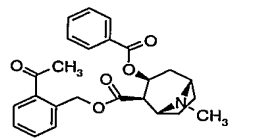
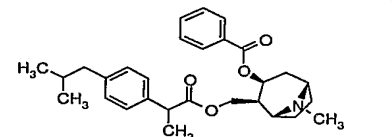
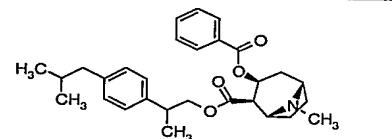
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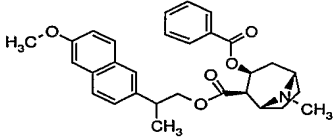
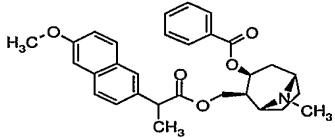
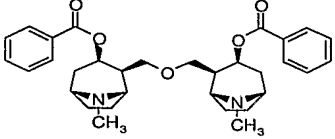
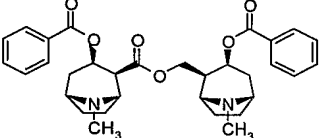
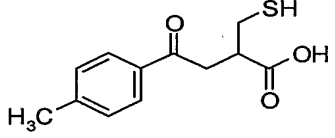
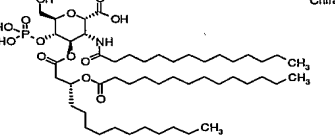
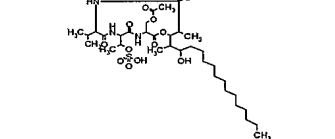
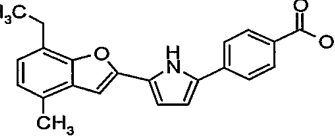
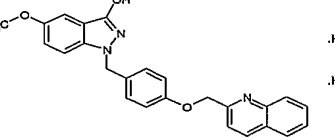
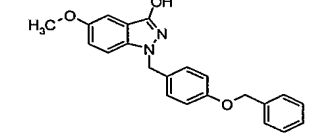
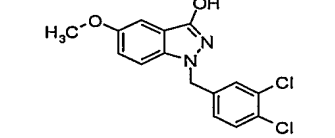
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1058		Leo		WO 9502577
1059		Kyorin	Kono, Y. et al. 115th Annu Meet Pharmaceut Soc Jpn (March 29-31, Sendai) 1995, Abst 30 (A3) 10-3.	EP 538477
1060		Abbott GmbH		WO 9500507
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1065		Bayer		US 5411960
1066		Baxter	France, C.P. et al. Drug Develop Res 1995, 35: 49.	EP 396282

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1105		Sankyo	Shiozaki, M. et al. Tetrahedron Lett 1996 37(40): 7271.	
1106		Nippon Kayaku		JP 96283290
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